

<hr/>					
EMBL; Z15028; CAA78747.1; -;	-				
DR EMBL; X64770; CAA46017.1; --	--				
DR PIR; S23543; S23543.	.				
DR Gramene; P30298; --	--				
DR InterPro; IPR001296; Glyco trans 1.	1.				
DR InterPro; IPR000368; Sucrose synth.	.				
DR Pfam; PRK0534; Glycosyltransf_1; 1.	1.				
DR Pfam; PRK0862; Sucrose synth; 1.	1.				
DR Transferase; Glycosyltransferase; Multigene family.					
KW CONFLICT 191 P -> L [IN REF. 2].	2.]				
FT					
SSO SEQUENCE 808 AA; 92113 MW; 3BF59E9886AB71 CRC64;					
<hr/>					
Query Match	70.7%;	Score 2983.5;	DB 1;	Length 808;	
Best Local Similarity	69.6%;	Pred No. 4 Se-131;			
Matches 559;	Conservative 103;	Mismatches 126;	Indels 15;	Gaps 3;	
<hr/>					
QY 3 HASGDVDETLHARNELVALLSKYVNKGKIQLPHHILDALDDEVQGSGRALAE-----	57				
DB : : : : : :					
QY 9 HSRERELGATFESSHPNELIALFSRYVNGQGMQLQRHQLLAED-----ALTEADKEK	60				
DB : : : : : :					
QY 58 -GFSLDVLRSAQAIVLPFPVAATAVRPRPGVWEYRVNVNHELSEVEQLTYSYEYLFKFKELV	116				
DB : : : : : :					
QY 61 YAFPEILLRAQAQAVLPPWVALAIRPFGWDYIRVNVSELAVEELSVEYLAFKSQLV	120				
DB : : : : : :					
QY 117 DGHNDPYVELDFEPNVSPNRSSSTGNVGQFLNRHLSSIMFNRRDCLEPLDLPLR	176				
DB : : : : : :					
QY 121 DGHTNSNFVELDFEPNPASFPSPMSKISGVQFLNRHLSSKLFOCKESLYELMLFLK	180				
DB : : : : : :					
QY 177 GHRKHGHVMNLNRIQSLGRLOSVLTKAEHLSKLPADTPYSOFAYAKFOEWGLEKGGWDT	236				
DB : : : : : :					
QY 181 AENHKGTMPNDRIQSRLGLSSLRKAEYLMGIPODTPSEFNHFQELGLEKGGWDC	240				
DB : : : : : :					
QY 237 AGHVLEMIHLLLDIIQAPDSPTLEKPIGRIPMIFNVVVSPHGYPGQANVLGLDTGGQI	296				
DB : : : : : :					
QY 241 AKRVLDITHLLDLLEAPDPANLEKFLGTIPMFENVWLSPHGFAQSNVLGYDPTGGQV	300				
DB : : : : : :					
QY 297 VYILDQVRALENEMVLKKOGLDVSPKILVTRLIPDAKTSCNORLERISGTOHTVIL	356				
DB : : : : : :					
QY 301 VYILDQVRALENEMLRIKOGLDIITPKILLVTRELPDAVGTTCQORVKYVIGTEHTIL	360				
DB : : : : : :					
QY 357 RVPFRNENGILKKWISRFVDVWPVYLETAEDAAGSIAAELQCTPDITIGNYSDGMVLASLL	416				
DB : : : : : :					
QY 361 RVPFPSENGILRKWISRFDVWPVFLETVEDVANEIMREQAKPOLIIGNYSDGNLVATLL	420				
DB : : : : : :					
QY 417 SYXWGLITQCNIHALEKTKYPDSDIFWNKFEKVFHSQCFQTADIAMNADFIITSTVOE	476				
DB : : : : : :					
QY 421 AHKLGVITQCTIHALEKTKPNSDIYLDKFDVSQFHFSQCFQTADLIAMNTDFIITSTVOE	480				
DB : : : : : :					
QY 477 IAGSKNTVGQYESHTAFTPLGLYRVWHGIDVDPKFNIVSPGADMSTIYPPTHEKAKRUTS	536				
DB : : : : : :					
QY 481 IAGSKDTVGQYESHTAFTPLGLYRVWHGIDVDPKFNIVSPGADMSTVTFPTHEADKRUTA	540				
DB : : : : : :					
QY 537 LHGSIEMLIYDPEQNDEHHGLHDORSKPILFSMARLDRVKNITGVEAFACAKRELNV	596				
DB : : : : : :					
QY 541 FHPBIEELLYSEVENDEHKFVLKOKNKPLIFSMAKLRVKNMGLUVMYGNKAHLRDLAN	600				
DB : : : : : :					
QY 597 LVVVAGYNDVNKSDDREBIABIKXHELIKTNHLPFGQFWISAOQTNRAUNGELYHYIADT	656				
DB : : : : : :					
QY 601 LIVICG-DHGNQSKDREEQASFQKWYGLIDQYKLGKHIRWISAQMNRVNGELYRYICDT	659				
DB : : : : : :					
QY 657 HGAFVQPALYEAFLTVTEAMTCGLPTATLHGCPAEIIIEHCVSGFHIDPVHPEQAVNLX	716				
DB : : : : : :					
QY 660 KGVFVQPAFYAFLGTVTEAMTCGLPTATCHGGPAEIIIDVGVSGHIIDPTHSHDKRADII	719				
DB : : : : : :					
QY 717 ADFFDRCKQDDPHWVNISGAGLQRITYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLTR	776				
DB : : : : : :					
QY 720 VNFFPKCKQDSTYNWINSUGGIQRTYFKYTWKLYSERLMTLAGVYGFWKYVSNLCERRTR	779				
DB : : : : : :					

RESULT 12
SUS3_ORYSA STANDARD; PRT; 816 AA.
AC Q43009;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase 3 [EC 2.4.1.13] (Sucrose-UDP glucosyltransferase 3).
GN SS3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Tainong 67; T-SUSE=Leaf, and Root;
RX MEDLINE=97076616; PubMed=9063969;
RA Huang J.W., Chen J.T., Yu M.P., Shyur L.F., Wang A.Y., Sung H.Y.,
Lee P.D., Su J.C.;
RA "Complete structures of three rice sucrose synthase isogenes and
RT differential regulation of their expressions.";
RL Biosci. Biotechnol. Biochem. 60:233-239(1996).
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC
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CC
CC EMBL; L03366; AAC41682.1; -.
DR Gramene; O43009; -.
DR InterPro; IPR001296; Glyco trans 1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos. transf. 1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
DR Transferrase; Glycosyltransferase; Multigene family.
SQ SEQUENCE 816 AA; 93209 MW; 4B5817C106A77D2A CRC64;

Query Match 69.98; Score 2948; DB 1; Length 816;
Best Local Similarity 68.24; Pred. No. 1.1e-188;
Matches 544; Conservative 119; Mismatches 133; Indels 2; Gaps 2;

QY 3 HADGRVEETLHARNELVALLSKYVKNKGILQPHHILDALDEVQSGGR-ALAEQPF 61
DB 14 HSWRERIGDSLSAHTNELVAFSLVQNGKGLQPHQIIAEYNAAIPEGEREKLDSALE 73

QY 62 DVLRSAGEAIVLPFVAIAVRPGVWYKRVNWHLSVQLTVSEYLRFKBELVDGQHN 121
DB 74 DVLRGAGEAIVPWIATLRPRGVWYLRINVSQGVPELSVPEYLFQKEQLVDGSTQ 133

QY 122 DPVYLEDFEPFNVSVPNPNRSSISNGVQFLNHLSSIMFERNDCLEPLDLRGRHK 181
DB 134 KNFVLELDFEPFNASFRPSLSKSGVQVQFLNHLSSKLFHDKESMPLNFRANRYK 193

QY 182 GHVWMLNDRIOSGLRSLVTKAEHLSKLPADTPYSQFAYKFOEWGLEKCGDGTAGHVL 241
DB 194 GWTWMLNDRISSLALQALRAKAEKHLAGITADTPYSEFHFHFQELGLEKCGCAQRVR 253

QY 242 EMHLLLDIIQAPDSTLEKELGIPMIFNVVSPHGYFQGANVLGIPDTGGQIVILD 301
DB 254 ETIHLLDLEAPESALEKELGIPMIFNVVSPHGYFQGANVLGIPDTGGQIVILD 313

QY 302 QVRALENEXVLRKQGLDVSFKILIVTRLPDAKGISCNQRLERISGTQHTYILVRPFR 361

Db 314 QVRAMENMLRIKQOGLNITPRILIVTRLLPDAHGTTCGRLEKVLGTEHTHILAVPR 373
QY 362 NENGILKKWISRPDVPWPLYLETFAEDAAGIAELAQCTPDFFIIGNYSDGNLVALSYKMG 421
Db 374 TENGTVRKWISRFVWPVLYETDVAHAEISGELQATPDLLIIGNYSDGNLVRCLLAKLG 433
QY 422 ITQCNIAHALEKTKYPSDIFWKNFDEKHFSCQFTADIIAMNADFIITSTYOEIAGSK 481
Db 434 VTHTCTIAHALEKTKYPSNLDLYWKKFEDHFFSCQFTADIIAMNADFIITSTYOEIAGSK 493
QY 482 NTWGVQESHATAFLGELYRVVHGIDVDFPKFNVSPGADMSIYFPHTKAKRUTSLFSGSI 541
Db 494 ETVGVQESHATAFLGELYRVVHGIDVDFPKFNVSPGADMSIYFPHTKAKRUTSLFSGSI 553
QY 542 ENLIYDPEQNDHGHLDHRSKPIELSMARLORVKNITGLVEAFKAKLRELNLVVA 601
Db 554 EELLPSDVENTEKFVLDKDKKPIELSMARLORVKNITGLVEAFKAKLRELNLVVA 613
QY 602 GYNDVNSKORDEIAEIKWHELIKTNLFGQFWMISACTNARNGELVRYIADTHGAFV 661
Db 614 G-DHGKESKDEKQAEAFKQKQENLIEQYNLNGHIRWISAQNRVRNGELVRYICDMGAFV 672
QY 662 QPALYEAFLGTVVEMTQGLTFEATLHGPGPAEIIIEHGVSGFHIDPHYHPEQAVNLMA 721
Db 673 QPALYEAFLGTVVEMTQGLTFEATLHGPGPAEIIIEHGVSGFHIDPHYHPEQAVNLMA 732
QY 722 RCKQDPDHWNVISGAGLQRIYKYTWKYSERLMTLAGVYGFWKYKSLERLETRVLEM 781
Db 733 KCQEDPNHWIKISQGGLORIEKYTWKYSERLMTLAGVYGFWKYKSLERLETRVLEM 792

QY 782 FYILKPRELAKTVPLAID 799
Db 793 LYALKYRKQATVPLAIE 810

RESULT 13
SUS1_SOLTU STANDARD; PRT; 805 AA.
ID -SUS1_SOLTU AC P10691;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase)
DE (SS16).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OX NCBI_TaxID=4113;
OX [1].
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sirtema;
RX MEDLINE=86152501; PubMed=2964386;
RA Salanoubat M., Belliard G.;
RT "Molecular cloning and sequencing of sucrose synthase cDNA from
RT potato (Solanum tuberosum L.): preliminary characterization of
RT sucrose synthase mRNA distribution.";
RL Gene 60:47-56(1987).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=cv. FL1607; TISSUE=Leaf;
RX MEDLINE=96172787; PubMed=8589622;
RA Fu H., Park W.D.;
RT "Sink- and vascular-associated sucrose synthase functions are encoded
RT by different gene classes in potato.";
RL plant Cell 7:1369-1385(1995).
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- TISSUE SPECIFICITY: Expression is at least 10 fold higher in
CC tubers compared to photosynthetically active tissues.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant


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CC sucrose synthase subfamily.
CC -----
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CC -----
DR EMBL; M18745; AAA33841.1; -
DR EMBL; U24C87; AAA97571.1; -
DR PIR; A29615; YUPOS.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
KW Transferase; Glycosyltransferase; Multigene family.
FT CONFLICT 221 221 KD -> D (IN REF. 2).
FT CONFLICT 731 732 XD -> RE (IN REF. 2).
FT CONFLICT 741 741 M -> T (IN REF. 2).
FT CONFLICT 748 748 E -> Q (IN REF. 2).
FT CONFLICT 759 759 S -> R (IN REF. 2).
SQ SEQUENCE 805 AA; 92416 MW; C453363A7CD32869 CRC64;

Query Match 69.8%; Score 2944.5; DB 1; Length 805;
Best Local Similarity 68.9%; Pred. No. 1.8e-188;
Matches 549; Conservative 115; Mismatches 132; Indels 1; Gaps 1;

QY 3 HASGDRVEDTTHAHNELVALLSKYVNGKGILOPHILDALDVEQSGGRALAEQGFILD 62
DB 10 HSLRVDATLAHRNEILLFLSRIESHGKILKPHELLAFDAIRQDDKKNLNEHAFEE 69

QY 63 VLRSQAQAIPLPPVAIAVRPRPGWVEYRVNHNHLSVEQLTVSEYLRKFKEELVDGQND 122
DB 70 LLKSTQEAIVLPPWVALAIRLRPGWVEYRVNHNHLSVEQLTVSEYLRKFKEELVDGASNG 129

QY 123 PYVLELDEPEPNVSPRNRSSISGNGVQFNLNHLSSIMFRNRCLEPLDLFGRHRKG 182
DB 130 NFVLELDEPEFTAPFPKPTLTGKISGNGVEFNLNHLSSIMFRNRCLEPLDLFGRHRKG 189

QY 183 HVMMLNDRIQSLGRLQSVLTAKAEHLSKLPADTPYSQFAYKPFQEWGLEKMGWDTAGHVLE 242
DB 190 KTWMLNDRIQSNLTQNLVLRKAEYILMLPETYPFEHFKFQILGKMGWDTAERVLE 249

QY 243 MIHLLEDICAPDSTLEKFLGRIPMIPNVVWVSPHGYFGQANVLGLPDTGQIVYILDQ 302
DB 250 MVMCLLDLEAPDSCTLEKFLGRIPMIPNVVWVSPHGYFGQANVLGLPDTGQIVYILDQ 309

QY 303 VRALENEMVLRLKKQGLDVSPIKILVTRLPDAGTSCNQLERISGTHYTLRVRPN 362
DB 310 VEAREREMLRKKEQGLDIIPRILIVTKLLDPDVGTTGQRIKRYGAHHILRVFPRT 369

QY 363 ENGLIKKWSRFQWVMPYLETPAEADAAGEIAELAQCTPDIIGNYSDGNLVASLSYKMG 422
DB 370 EKGIVRWISSEFYKPYMETFIEDVAKESIAELQAKEDLLIGNYSEGNLAASLLAHKLV 429

QY 423 TQCNIAHALEKTKPDSDIIFWNFDEKHFSCQFTADLIANNADFIITSTYQEIAGSKN 482
DB 430 TQCTIAHALEKTKPDSDIYWKKEDEKHFSSQFTADLIANNHDFIITSTFQETAGSKD 489

QY 483 TVGOYESHATPLGLVVRVHGIVDEPKNIVSPGADMSIYFEPTEKAKELTSLHGSIE 542
DB 490 TVGOYESHMAFTMPLGVVRVHGIVDEPKNIVSPGADINLYFSYTEKELTAFHPHID 549

QY 543 NLIYDPEONDEHIGLDRSKPIFSMARLDRVKNITGLVEAFKAKAKMLRVLNVLVWAG 602
DB 550 ELLYSVDENDEHLVLRDRTXPLFTARLDRVKNITGLVEYAKNPLRGLVNLVWVG 609

QY 603 YNDVKNKOREEIAIEKQHELIKTNLFGQFRNISAQTNARNSELYRYIACTHGAFFVQ 662
DB 610 -DRRKESKLEQAEQKMKVYELIETHNLNGQFRWISSQNRVNRNCELYRYIADTKGAPVQ 668

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QY 663 PALYEAEGLTVVEAWTCGLPTFATLHGPGAKLIEHGVSGFHIDPYPHPOAVNLMADEPDR 722
DB 669 PAFYEAEGLTVVEAWTCGLPTFATNHHGPAELIIVHGKSGFHIDPYPHPOARLLADFEK 728

QY 723 CKQDPDFHWNISGAGLQRIYKYTKIYSERIMTLAGYVGFYKVKYKLERLETRYLEMF 782
DB 729 CKQDPSEHWTISMGGLKRIEIKYTKIYSESLTLAAVYGFYKVKYKLERLETRYLEMF 788

QY 783 YILFRELAKTVPLAID 799
DB 789 YALKYRKMAEAVPLAAE 805

RESULT 14
SUSY_LYCES STANDARD; PRT; 805 AA.
AC P49037;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) [Sucrose-UDP glucosyltransferase].
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_taxID=4281;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VF36; TISSUE=Pistil;
RX MEDLINE=94120019; PubMed=8290642;
RT Wang F., Smith A.G., Brenner M.L.;
RL Plant Physiol. 103:1463-1464(1993).
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC -----
DR EMBL; L19762; AAA34196.1; -
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 805 AA; 92446 MW; 8C7CCB09415483F5 CRC64;

Query Match 69.8%; Score 2944.5; DB 1; Length 805;
Best Local Similarity 69.0%; Pred. No. 1.8e-188;
Matches 550; Conservative 114; Mismatches 132; Indels 1; Gaps 1;

QY 3 HASGDRVEDTTHAHNELVALLSKYVNGKGILOPHILDALDVEQSGGRALAEQGFILD 62
DB 10 HSLRVDATLAHRNEILLFLSRIESHGKILKPHELLAFDAIRQDDKKNLNEHAFEE 69

QY 63 VLRSQAQAIPLPPVAIAVRPRPGWVEYRVNHNHLSVEQLTVSEYLRKFKEELVDGQND 122
DB 70 LLKSTQEAIVLPPWVALAIRLRPGWVEYRVNHNHLSVEQLTVSEYLRKFKEELVDGASNG 129

QY 123 PYVLELDEPEPNVSPRNRSSISGNGVQFNLNHLSSIMFRNRCLEPLDLFGRHRKG 182
DB 130 NFVLELDEPEFTAPFPKPTLTGKISGNGVEFNLNHLSSIMFRNRCLEPLDLFGRHRKG 189

QY 183 HVMMLNDRIQSLGRLQSVLTAKAEHLSKLPADTPYSQFAYKPFQEWGLEKMGWDTAGHVLE 242

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Db 190 KTWMLNDRIHNSNTLQNLVLRKABEYLIMLPETPFEEHKEFQELGLEKMGWDTAERVLE 249
 Qy 243 MIHLLLDIIQAPDSTLEKELGRIPMLFNVVVSPHGYFGQANVLGPDGTGGQIVYILDQ 302
 Db 250 MWCMLLDLEAPDSTLEKELGRIPMLFNVVVSPHGYFGQANVLGPDGTGGQIVYILDQ 309
 Qy 303 VRALENEMVRLKKGGLDVSPKILIVTRLIPDAGTSCNORLERISGTOHTYILRVFERN 362
 Db 310 VPAJEREMLRKIKKQGLDITPRIIDIVTRLIPDAGTSCNORLERISGTOHTYILRVFERN 369
 Qy 363 ENGLKWKWISRFDPVWPYLETFAEDAAGEIAAELQCTPDIIGNYSNGLVASLISYKMG 422
 Db 370 EKGIVRWISRFDPVWPYLETFAEDAAGEIAAELQCTPDIIGNYSNGLVASLISYKMG 429
 Qy 423 TQCNIAHALEKTKYPDSDIIPWKNDEKXHFSCQTAADIIMNADFIITSTYQBIAGSKN 482
 Db 430 TQCTIAHALEKTKYPDSDIIPWKNDEKXHFSSQCTADLIAMNHTDFIITSTYQBIAGSKN 489
 Qy 483 TVGQYESHATAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKELTSLHGSIE 542
 Db 490 TVGQYESHATAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKELTSLHGSIE 549
 Qy 543 NLIYDPEQNDHEHIGLHSDRSKPIILFSMARLDRVKNITGLVEAFKAKRELNLVNVVAG 602
 Db 550 ELLYSYDVNDHEHIGLHSDRSKPIILFSMARLDRVKNITGLVEAFKAKRELNLVNVVAG 609
 Qy 603 YNDVNSKDRBEIAIEKHELIKTHNLFCQFRWISAOQNARNGELYRIYADTHGAFVQ 662
 Db 610 -DRKESKDLFEKAEKMKYELIETIKNGQFRWISSQMNVRNGELYRIYADTHGAFVQ 668
 Qy 663 PALYEAAGLTWVEAMTGLPTFATLHGSPABIIIEHGVSGPHIDPVHPQAVNLMDPDR 722
 Db 669 PALYEAAGLTWVEAMTGLPTFATLHGSPABIIIEHGVSGPHIDPVHPQAVNLMDPDR 728
 Qy 723 CKQDPDHWNVISGAGLQRIYKTYKILYSERLMTLAGYGVFWKYSKLERLTRYLEM 782
 Db 729 CKQDPDHWNVISGAGLQRIYKTYKILYSERLMTLAGYGVFWKYSKLERLTRYLEM 788
 Qy 783 YILKRELAKTVPLAID 799
 Db 789 YALKYRWAEAVPLAAE 805

RESULT 15

SUSY_VICFA STANDARD; PRT; 806 AA.
 AC P31926;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sucrose synthase [EC 2.4.1.13] (Sucrose-UDP glucosyltransferase).
 GN SUCS.
 OS Vicia faba (Broad bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Papilionoideae; Viciae; Vicia.
 OX NCBI_TaxID=3906;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Fzibo;
 RX MEDLINE=93379571; PubMed=7764025;
 RA Heim U., Weber H., Baumein H., Wobus U.;
 RA "A sucrose-synthase gene of Vicia faba L.: expression pattern in
 RT developing seeds in relation to starch synthesis and metabolic
 RT regulation.";
 RL Planta 191:394-401(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Kleine Thueringer; TISSUE=Root nodules;
 RX MEDLINE=94003420; PubMed=840379;
 RA Kuster H., Fruhling M., Perlick A.M., Puchler A.;
 RA "The sucrose synthase gene is predominantly expressed in the root
 RT nodule tissue of Vicia faba.";

RL Mol. Plant Microbe Interact. 6:507-514(1993).
 CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
 CC fructose for various metabolic pathways.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
 CC -!- SIMILARITY: Belongs to the glucosyltransferase family 1. Plant
 CC sucrose synthase subfamily.
 CC -----
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 CC -----
 DR EMBL; X69773; CA49428.1; -;
 DR EMBL; M97551; AAC37346.1; -;
 DR PIR; S31479; S31479.
 DR InterPro; IPR001296; Glyco_trans_1.
 DR InterPro; IPR000368; Sucrose_synth.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 DR Pfam; PF00862; Sucrose_synth; 1.
 KW Transferase; Glycosyltransferase.
 SQ SEQUENCE 806 AA; 92520 MW; A54B004C0732F306 CRC64;
 Query Match 69.8%; Score 2944.5; DB 1; Length 806;
 Best Local Similarity 68.8%; Pred. No. 1.8e-188;
 Matches 549; Conservative 122; Mismatches 126; Indels 1; Gaps 1;
 Qy 3 HASGREDYDTHAHRNELVALLSKYVNGKGILOPHHLDALDEVQSGGRALAEGLFD 62
 Db 10 HSLRLEDTLTANRNEITALLSRIEAKGKILQHQHVIABEPIEENRQKLTGATGE 69
 Qy 63 VLRSQAQAVILPPVATAVRRPGVWYVRVNVHLSVQSLTVSEYLFKELVDQND 122
 Db 70 VLRSQAQAVILPPVATAVRRPGVWYVRVNVHLSVQSLTVSEYLFKELVDQND 129
 Qy 123 PYVLELDFEPNVSPRPNRSSISNGVQFNRHLSSIMFRNDCLEPLDPLRCHRGK 182
 Db 130 NFVLELDFEPNVSPRPNRSSISNGVQFNRHLSSIMFRNDCLEPLDPLRCHRGK 189
 Qy 183 HVMLNDRIQSLGRLOSVLTAKBEHLSKLPADTPYSQFAYKFOEWGLEKMGDTAGHVLE 242
 Db 190 KTMINDRIQNPDSILQHVLRKAEVLTVDPTETPYSEFEHRFQELGLERGMGDSAEVLE 249
 Qy 243 MIHLLLDIIQAPDSTLEKELGRIPMLFNVVVSPHGYFGQANVLGPDGTGGQIVYILDQ 302
 Db 250 SIQLELDLEAPDSTLEKELGRIPMLFNVVVSPHGYFGQANVLGPDGTGGQIVYILDQ 309
 Qy 303 VRALENEMVRLKKGGLDVSPKILIVTRLIPDAGTSCNORLERISGTOHTYILRVFERN 362
 Db 310 VRALENEMVRLKKGGLDVSPKILIVTRLIPDAGTSCNORLERISGTOHTYILRVFERN 369
 Qy 363 ENGLKWKWISRFDPVWPYLETFAEDAAGEIAAELQCTPDIIGNYSNGLVASLISYKMG 422
 Db 370 EKGIVRWISRFDPVWPYLETFAEDAAGEIAAELQCTPDIIGNYSNGLVASLISYKMG 429
 Qy 423 TQCNIAHALEKTKYPDSDIIPWKNDEKXHFSCQTAADIIMNADFIITSTYQBIAGSKN 482
 Db 430 TQCTIAHALEKTKYPDSDIIPWKNDEKXHFSCQTAADIIMNADFIITSTYQBIAGSKN 489
 Qy 483 TVGQYESHATAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKELTSLHGSIE 542
 Db 490 TVGQYESHATAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKELTSLHGSIE 549
 Qy 543 NLIYDPEQNDHEHIGLHSDRSKPIILFSMARLDRVKNITGLVEAFKAKRELNLVNVVAG 602
 Db 550 ELLYSYDVNDHEHIGLHSDRSKPIILFSMARLDRVKNITGLVEAFKAKRELNLVNVVAG 609
 Qy 603 YNDVNSKDRBEIAIEKHELIKTHNLFCQFRWISAOQNARNGELYRIYADTHGAFVQ 662
 Db 610 -DRKESKDLFEKAEKMKYELIETIKNGQFRWISSQMNVRNGELYRIYADTHGAFVQ 668

QY	663	PALYEPGLTVVEAMTCGLPTEATLHGGPAEIIIEHGVSGFHIIDPYHPEQAVNLMADFEER	722
Db	669	PAVEAFGLTVVEAMATGLPTEATLHGGPAEIIIVHKSGFHIIDPYHGRADLLVEFEK	728
QY	723	CKQDPDHWNNISGAGLQRIYKYTWKIYSERLMTLAGVYGFVKYVSKLERLETERYLEMF	782
Db	729	VKADPSHWDKISLGGLQRIEKEYTWQIYSORLLTLTGTVYGFVKHVSNDRLERSRYLEMF	788
QY	783	YILKRELAKTVPILAIDQ	800
Db	789	YALKYRXIAESVPLAVEE	806

Search completed: May 24, 2004, 11:27:59
Job time : 16.9392 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:38 ; Search time 40.8218 Seconds
(without alignments)
6198.778 Million cell updates/sec

Title: US-10-080-114a-2

Perfect score: 4217

Sequence: 1 STHASGRVEDTLAHRNEL.....YILKRELAKTVLAIDQPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4186	99.3	796	10	Q93WS3 zea mays (m
2	4178	99.1	809	10	Q8L5H0 zea mays (m
3	3523	83.5	811	10	Q9SLY2 citrus unsh
4	3506	83.1	811	10	Q9SLV8 citrus unsh
5	3456	82.0	809	10	Q9ML11 arabidopsis
6	3396	80.5	812	10	Q9FRX3 pyrus pyrif
7	3377	80.1	811	10	Q84T18 solanum tub
8	3366	79.8	808	10	Q9SBD5 arabidopsis
9	3297	78.2	822	10	Q94G60 beta vulgar
10	3263	77.4	811	10	Q9ZPC5 craterostig
11	3117	73.9	809	10	Q9ZPC6 craterostig
12	2998.5	71.1	806	10	Q9SBL8 citrullus l
13	2991	70.9	816	10	Q8W1W4 bambusa old
14	2984.5	70.8	805	10	Q9SL52 citrus unsh
15	2982.5	70.7	808	10	Q8W1W3 bambusa old
16	2982	70.7	816	10	Q43706 zea mays (m

17	2968.5	70.4	805	10	Q9SLY1 citrus unsh
18	2968.5	70.4	808	10	Q8W1W2 bambusa old
19	2967.5	70.2	802	10	Q9LKR0 saccharum o
20	2961	70.2	806	10	Q9XGB7 gossypium h
21	2958	70.1	816	10	Q8LJT5 oncidium cv
22	2954	70.0	816	10	Q8LJT4 x mokara cv
23	2953	70.0	816	10	Q8GS23 oryza sativ
24	2944.5	69.8	805	10	Q7Y078 solanum tub
25	2943.5	69.8	805	10	Q82693 lycopersico
26	2943.5	69.8	806	10	Q9TOM9 pisum sativ
27	2937.5	69.7	804	10	Q9AVR8 pisum sativ
28	2936.5	69.6	806	10	Q81610 pisum sativ
29	2934.5	69.6	805	10	Q9TOM6 medicago tr
30	2933.5	69.6	815	10	Q43223 triticum ae
31	2929.5	69.5	803	10	Q9LW57 chenopodium
32	2925.5	69.4	805	10	Q9XG65 medicago tr
33	2924.5	69.4	805	10	Q8GT43 phaseolus v
34	2919.5	69.2	805	10	Q84UC3 solanum tub
35	2913.5	69.1	805	10	Q82691 lycopersico
36	2904.5	68.9	808	10	Q9LXL5 arabidopsis
37	2892.5	68.6	808	10	Q82073 triticum ae
38	2340.5	55.5	942	10	Q9FX32 arabidopsis
39	2310.5	54.8	887	10	Q9FHU4 arabidopsis
40	2259.5	53.6	798	10	Q7XNX5 oryza sativ
41	2251.5	53.4	798	10	Q7XXL1 oryza sativ
42	2125	50.4	794	16	Q820M5 nitrosomona
43	2093.5	49.6	532	10	Q94CC8 arabidopsis
44	1841.5	43.7	808	16	Q8DK23 synechococc
45	1833	43.5	806	2	Q9ZEV2 anabaena sp

ALIGNMENTS

RESULT 1

Q93WS3	PRELIMINARY;	PRT;	796 AA.
ID	Q93WS3		
AC	Q93WS3;		
DT	01-DEC-2001 (TRENBLrel. 19, Created)		
DT	01-DEC-2001 (TRENBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (TRENBLrel. 24, Last annotation update)		
DE	Sucrose synthase (Fragment).		
OS	Zea mays (Maize).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.		
OX	NCBI_TaxID=4577;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Root;		
RA	Carlson S.J., Chourey P.S., Helentjaris T., Datta R.;		
RT	"Gene expression studies on developing kernels of maize sucrose		
RL	synthase (SuSy) mutants show evidence for a third SuSy gene."		
RL	Plant Mol. Biol. 0:0-0(2001).		
DR	EMBL; AY059416; AAL27096.1; -		
DR	GO; GO:0009058; P:biogenesis; IEA.		
DR	GO; GO:0005985; P:sucrose metabolism; IEA.		
DR	InterPro; IPR001296; Glyco_transf.		
DR	InterPro; IPR00368; Sucrose synth.		
DR	Pfam; PF00534; Glycose_transf_1; 1.		
DR	Pfam; PF00862; Sucrose_synth; 1.		
FT	NON_TER		
SQ	SEQUENCE 796 AA; 90453 MW; 7E7A92CB0C31F898 CRC64;		

Query Match 99.3%; Score 4186; DB 10; Length 796;
Best Local Similarity 100.0%; Pred. No. 1.2e-300;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DEVEDTLAHRNELVALLSKYVNGKGLIOPHHILDALDEVQSGGERALAEQPFLLDLRS 66

DB 1 DEVEDTLAHRNELVALLSKYVNGKGLIOPHHILDALDEVQSGGERALAEQPFLLDLRS 60

QY 67 AQEATVLPFVAIAVRPRPGWWEYVRVNVNHELVSQELTVSEYLRFRKEELVDGQNDPPYL 126

Db 61 AQAELVLPFPVAIAVRPPGVWEYVRVNVHLSVEQLTVSEYLRFKBELVQGHNDPYVL 120
 QY 127 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDCLEPLDPLFLGRHHRKHGHWMM 186
 Db 121 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDCLEPLDPLFLGRHHRKHGHWMM 180
 QY 187 LNDRTQSLGRQSVLTAKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 246
 Db 181 LNDRTQSLGRQSVLTAKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 240
 QY 247 LLDIIQAPDPSLTLEKFLGRIPMFENVVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 306
 Db 241 LLDIIQAPDPSLTLEKFLGRIPMFENVVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 300
 QY 307 ENEMVLRLKKQGLDVSFKLIVTRLIPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 366
 Db 301 ENEMVLRLKKQGLDVSFKLIVTRLIPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 360
 QY 367 LKKNISRDVWPVLETFEADAAAGEIAAELOQTGPDFTIIGNYSDGNLVASLLSYKMGITQCN 426
 Db 361 LKKNISRDVWPVLETFEADAAAGEIAAELOQTGPDFTIIGNYSDGNLVASLLSYKMGITQCN 420
 QY 427 IAHALEKTYPDSDI FWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 486
 Db 421 IAHALEKTYPDSDI FWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 480
 QY 487 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLHGSINLIY 546
 Db 481 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLHGSINLIY 540
 QY 547 DPEONDEHGHLDLDRSKPILFMSARLDVKNITGLVEAFKAKRELNVLVVAGYNDV 606
 Db 541 DPEONDEHGHLDLDRSKPILFMSARLDVKNITGLVEAFKAKRELNVLVVAGYNDV 600
 QY 607 NKSQKREIEAIEKMHLEIKTNLFGQFRWISQATNRANGELYRYIADTHGAFVQPALY 666
 Db 601 NKSQKREIEAIEKMHLEIKTNLFGQFRWISQATNRANGELYRYIADTHGAFVQPALY 660
 QY 667 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDPYHPPEQAVNLMADFFDRCKQD 726
 Db 661 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDPYHPPEQAVNLMADFFDRCKQD 720
 QY 727 PDHWNVISAGLQRIYKTYKWTWYSRLMTLAGYGVGFVKVSKLERLETTRYLEMFIYK 786
 Db 721 PDHWNVISAGLQRIYKTYKWTWYSRLMTLAGYGVGFVKVSKLERLETTRYLEMFIYK 780
 QY 787 FRELAKTVPLAIDQPQ 802
 Db 781 FRELAKTVPLAIDQPQ 796

RESULT 2

Q8L5H0 PRELIMINARY; PRT; 809 AA.
 ID Q8L5H0
 AC Q8L5H0
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 CS Sucrose synthase 3 (EC 2.4.1.13).
 DE Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 CX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=cv. Caramba; TISSUE=Anaerobic root;
 RA Holtgraeve D.L., Scholz A., Altmann B., Winter H.;
 RT "Complete coding sequence of a third sucrose synthase isoform in
 RT maize."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY124703; AA: M89473.1; "

DR GO: 0016157; P:sucrose synthase activity; IEA.
 DR GO: 0016757; P:transferase activity, transferring glycosyl...; IEA.
 DR GO: 0009056; P:biogenesis; IEA.
 DR GO: 0005985; P:sucrose metabolism; IEA.
 DR InterPro: IPR001296; Glyco trans 1.
 DR InterPro: IPR00368; Sucrose synth.
 DR Pfam: PF00534; Glycos transf 1; 1.
 DR Pfam: PF00862; Sucrose synth; 1.
 DR Transferrase; Glycosyltransferase.
 SQ SEQUENCE 809 AA; 51926 MW; 848FA01ADCC6C19 CRC64;

Query Match 99.1%; Score 4176; DB 10; Length 809;
 Best Local Similarity 99.7%; Pred. No. 4.7e-300;
 Matches 794; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 DRVEDTLAHARNELVALLSKYVNGKGILOPHHILDALDEVQSGGRALAEGLFVILRS 66
 Db 14 DRVEDTLAHARNELVALLSKYVNGKGILOPHHILDALDEVQSGGRALAEGLFVILRS 73
 QY 67 AQEAIVLPFPVAIAVRPPGVWEYVRVNVHLSVEQLTVSEYLRFKBELVQGHNDPYVL 126
 Db 74 AQEAIVLPFPVAIAVRPPGVWEYVRVNVHLSVEQLTVSEYLRFKBELVQGHNDPYVL 133
 QY 127 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDCLEPLDPLFLGRHHRKHGHWMM 186
 Db 134 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDCLEPLDPLFLGRHHRKHGHWMM 193
 QY 187 LNDRTQSLGRQSVLTAKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 246
 Db 194 LNDRTQSLGRQSVLTAKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 253
 QY 247 LLDIIQAPDPSLTLEKFLGRIPMFENVVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 306
 Db 254 LLDIIQAPDPSLTLEKFLGRIPMFENVVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 313
 QY 307 ENEMVLRLKKQGLDVSFKLIVTRLIPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 366
 Db 314 ENEMVLRLKKQGLDVSFKLIVTRLIPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 373
 QY 367 LKKNISRDVWPVLETFEADAAAGEIAAELOQTGPDFTIIGNYSDGNLVASLLSYKMGITQCN 426
 Db 374 LKKNISRDVWPVLETFEADAAAGEIAAELOQTGPDFTIIGNYSDGNLVASLLSYKMGITQCN 433
 QY 427 IAHALEKTYPDSDI FWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 486
 Db 434 IAHALEKTYPDSDI FWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 493
 QY 487 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLHGSINLIY 546
 Db 494 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLHGSINLIY 553
 QY 547 DPEONDEHGHLDLDRSKPILFMSARLDVKNITGLVEAFKAKRELNVLVVAGYNDV 606
 Db 554 DPEONDEHGHLDLDRSKPILFMSARLDVKNITGLVEAFKAKRELNVLVVAGYNDV 613
 QY 607 NKSQKREIEAIEKMHLEIKTNLFGQFRWISQATNRANGELYRYIADTHGAFVQPALY 666
 Db 614 NKSQKREIEAIEKMHLEIKTNLFGQFRWISQATNRANGELYRYIADTHGAFVQPALY 673
 QY 667 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDPYHPPEQAVNLMADFFDRCKQD 726
 Db 674 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDPYHPPEQAVNLMADFFDRCKQD 733
 QY 727 PDHWNVISAGLQRIYKTYKWTWYSRLMTLAGYGVGFVKVSKLERLETTRYLEMFIYK 786
 Db 734 PDHWNVISAGLQRIYKTYKWTWYSRLMTLAGYGVGFVKVSKLERLETTRYLEMFIYK 793
 QY 787 FRELAKTVPLAIDQPQ 802
 Db 794 FRELAKTVPLAIDQPQ 809

```
Q9SLY2 PRELIMINARY; PRT; 811 AA.
ID Q9SLY2
AC Q9SLY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update);
DE Sucrose synthase.
OS Citrus unshiu (satsuma orange).
GN Citrus unshiu (satsuma orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=55188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagawa-Wase; TISSUE=fruit;
RA Komatsu A.;
RT "Isolation of three sucrose synthase isoforms from Citrus.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022091; BAA88904.1; -.
DR GO; GO:0009058; P:biomethylation; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 811 AA; 92633 MW; 0682BAF7AAAB58F0 CRC64;

Query Match 83.5%; Score 3523; DB 10; Length 811;
Best Local Similarity 82.6%; Pred. No. 1.4e-251;
Matches 655; Conservative 70; Mismatches 56; Indels 2; Gaps 1;

QY 7 DRVEDTLHAHNEIVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 64
DB 14 ERVEDTLVHNEIVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 73
QY 65 RSAQEAIVLPFFVAIAVRPGWVEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 124
DB 74 KSAQEAIVLPFFVAIAVRPGWVEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 133
QY 125 VLELDFEPFNATPPRNRSSISNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 184
DB 134 VLELDFEPFNATPPRNRSSISNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 193
QY 185 MMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFGWGLKMGDTAGHVLMI 244
DB 194 LMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFGWGLKMGDTAGHVLMI 253
QY 245 HLLDIIQADPPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 304
DB 254 HLLDIIQADPPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 313
QY 305 ALENEMVLRLKKGGLDVSPKILIVTRLPDAGTSCNQLRERISGTOHTYILRVPRNEN 364
DB 314 ALENEMVLRLKKGGLDVSPKILIVTRLPDAGTSCNQLRERISGTOHTYILRVPRNEN 373
QY 365 GILKKWISRFDPVWPYLETFAEDAAGEIAAEIQLQGPDPFIIGNYSDGNLVAASLLYKMGITQ 424
DB 374 GILKKWISRFDPVWPYLETFAEDAAGEIAAEIQLQGPDPFIIGNYSDGNLVAASLLYKMGITQ 433
QY 425 CNIAHALEKTKYPSDIIKWKPFDEKHYKSCOPTADIIANNADFIITSTYQEIAGSKNTV 484
DB 434 CNIAHALEKTKYPSDIIKWKPFDEKHYKSCOPTADIIANNADFIITSTYQEIAGSKNTV 493
QY 485 QYTESHTAFTLPGLRVVGHGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSINL 544
DB 494 QYTESHTAFTLPGLRVVGHGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSINL 553
QY 545 IYDFEONDEHGHLDSDRSKPIVFSMARLDVKNITGLVFAFAKAKRELNLVNVVAGYN 604
DB 554 LFDPEONDEHGHLDSDRSKPIVFSMARLDVKNITGLVFAFAKAKRELNLVNVVAGYN 613
QY 605 DVNKSCKOREEIAEIKMELIKTNLFGQFPIWISQATNRANGELYRYIADTHGAFVQPA 664
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DB 614 DVNKSCKOREEIAEIKMELIKTNLFGQFPIWISQATNRANGELYRYIADTHGAFVQPA 673
QY 665 LYEAFLGTVVEAMTCGLPTATLHGGPAEIIHGVSGPHIDPYEPQAVNLMADFPDRCK 724
DB 674 FYEAFGLTVVEAMTCGLPTATLHGGPAEIIHGVSGPHIDPYEPQAVNLMADFPDRCK 733
QY 725 QDPHWNINISGAGIQRIVYKTYKISYERLMTLAGVYGFVWYVSKLETERRYLEMFYI 784
DB 734 ENPSHWKKISDGGUKRIYRTWKIYERLMTLAGVYGFVWYVSKLETERRYLEMFYI 793
QY 785 LKPRELAKTVPLA 797
DB 794 LKFRDLVKSUPLA 806

RESULT 4
Q9SLV8 PRELIMINARY; PRT; 811 AA.
ID Q9SLV8
AC Q9SLV8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update);
DE Sucrose synthase.
OS Citrus unshiu (satsuma orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=55188;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu A.;
RT "Cloning of sucrose synthase (CITSUSA) gene from Citrus.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025778; BAA88981.1; -.
DR GO; GO:0009058; P:biomethylation; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 811 AA; 92549 MW; E7868C77BD1E1B3E CRC64;

Query Match 83.1%; Score 3506; DB 10; Length 811;
Best Local Similarity 82.1%; Pred. No. 2.5e-250;
Matches 651; Conservative 72; Mismatches 58; Indels 2; Gaps 1;

QY 7 DRVEDTLHAHNEIVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 64
DB 14 ERVEDTLVHNEIVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 73
QY 65 RSAQEAIVLPFFVAIAVRPGWVEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 124
DB 74 KSAQEAIVLPFFVAIAVRPGWVEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 133
QY 125 VLELDFEPFNATPPRNRSSISNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 184
DB 134 VLELDFEPFNATPPRNRSSISNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 193
QY 185 MMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFGWGLKMGDTAGHVLMI 244
DB 194 LMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFGWGLKMGDTAGHVLMI 253
QY 245 HLLDIIQADPPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 304
DB 254 HLLDIIQADPPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 313
QY 305 ALENEMVLRLKKGGLDVSPKILIVTRLPDAGTSCNQLRERISGTOHTYILRVPRNEN 364
DB 314 ALENEMVLRLKKGGLDVSPKILIVTRLPDAGTSCNQLRERISGTOHTYILRVPRNEN 373
QY 365 GILKKWISRFDPVWPYLETFAEDAAGEIAAEIQLQGPDPFIIGNYSDGNLVAASLLYKMGITQ 424
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DB 374 GILRQWISFDVWPYLETETEDVSGSEITAELOQFPDFIIGNSDGNLVSLLAYKMGITQ 433
QY 425 CNIAHALEKTKYPSDIFWKNDEKHFSCQFADIIAMNADFIITSTYQEIAGSKNTV 484
DB 434 CTTAHALEKTKYPSDIYKWKFEKHFSCQFADIIAMNADFIITSTYQEIAGSKNTV 493
QY 485 GQYESHTAFTPLGXYRVHGDIVDFPKFNIIVSGADMSIYFPHTEKAKRLTSLHGSINL 544
DB 494 GQYESHTAFTPLGXYRVHGDIVDFPKFNIIVSGADMSIYFPHTEKAKRLTSLHGSINL 553
QY 545 IYVPEQNDHEHGLDHSRKLPSMARLDVKNITGLVFAFAKCAKLELWNLVVVAGYN 604
DB 554 LFDPEQNDHEHGLDHSRKLPSMARLDVKNITGLVFAFAKCAKLELWNLVVVAGYN 613
QY 605 DVNKSQDREIAIEKXHELIKTHNLPGQPRWISAOCTNRARNGELYRIYADTHGAFVQPA 664
DB 614 DVNKSQDREIAIEKXHELMKTKYKLDQGFNIAAQTNRARNGELYRIYADTHGAFVQPA 673
QY 665 LYBAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHDIDPHPEQAVNLMADFPDRCK 724
DB 674 FYBAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHDIDPHPEQAVNLMADFPDRCK 733
QY 725 QDPDHWNTISGAGLQRIYKTKYISERLMTLAGVYGFWKYVSKLELETRVLEMYI 784
DB 734 ENPSHWKISDGLKRIYKTKYISERLMTLAGVYGFWKYVSKLELETRVLEMYI 793
QY 785 LKFERELAKTVPLA 797
DB 794 PKFRDLVKSVPPLA 806

RESULT 5

Q9M111 PRELIMINARY; PRT; 809 AA.
AC Q9M111; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative sucrose synthetase (AT4G02280/T2H3_8).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN RN
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
Mayer K.F.X.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN RN
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
PL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN RN
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
Banno J., Bower L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karl-in-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN RN
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banno J., Banno F., Dale J.M.,
Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bower L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karl-in-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene AT4G02280 (GI:7268988)";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN RN
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W.,
Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C.,
Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W.,
Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL161494; CAB80721.1; -
DR EMBL; AY056784; AAL09730.1; -
DR EMBL; AY051001; AAK93678.1; -
DR EMBL; AY142511; AAN13112.1; -
DR PIR; B85029; B85029.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco trans 1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos transf_1; -
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 809 AA; 92002 MW; BC5151F2FBF265D5 CRC64;
Query Match 82.0%; Score 3456; DB 10; Length 809;
Best Local Similarity 79.9%; Pred. No. 1.2e-246;
Matches 635; Conservative 89; Mismatches 69; Indels 2; Gaps 1;
QY 7 DRVEDTLHAHRNELVALLSKYVNGKGILOPHHILDALDEVQSG--GRAAEQPFDLVL 64
DB 14 DRVQDTLSAHRNELVALLSKYVNGKGILOPHHILDALDEVQSG--GRAAEQPFDLVL 73
QY 65 RSAQEAIVLPFVAIAVRPGWWEYVYVNVHLSVEQLTVSEYLRKEELVDGQNDPY 124
DB 74 KSAMEALVWPPFVAIAVRPGWWEYVYVNVHLSVEQLTVSEYLRKEELVDGQNDPY 133
QY 125 VLEDDFPENVSVPNKRSSISGVGVQVFLNRLHSSIMFRNDCLEPLDFLRHHRKHGV 184
DB 134 CLEDDFPENVSVPNKRSSISGVGVQVFLNRLHSSIMFRNDCLEPLDFLRHHRKHGV 193
QY 185 MMINDRIQSLGRSLVITKAEEHLSKUPADTPYQPAYKFOEWLEKQWGTAGHLEMI 244
DB 194 LMLNDRIQSLGRSLVITKAEEHLSKUPADTPYQPAYKFOEWLEKQWGTAGHLEMI 253
QY 245 HLLDITIQADPDPSTLEKFLGRIPMIENVVVSHPGYFGQANVLGLPDTGGQIVYILDQVR 304
DB 254 HLLSDITIQADPDPSTLEKFLGRIPMIENVVVSHPGYFGQANVLGLPDTGGQIVYILDQVR 313
QY 305 ALENEMVLRKQGLDVSFKLIVITRLIPDAKGTSCNQLRERISGTQHTYILRVFPRNEN 364
DB 314 ALENEMVLRKQGLDVSFKLIVITRLIPDAKGTSCNQLRERISGTQHTYILRVFPRNEN 373
QY 365 GILKRWISRFVWPVPLETFAEADAAGEIAAEILOGPDPFIIGNYSDGNLVASLLSYKMGITQ 424
DB 374 GILKRWISRFVWPVPLETFAEADAAGEIAAEILOGPDPFIIGNYSDGNLVASLLSYKMGITQ 433
QY 425 CNIAHALEKTKYPSDIFWKNDEKHFSCQFADIIAMNADFIITSTYQEIAGSKNTV 484
DB 434 CTTAHALEKTKYPSDIYKWKFEKHFSCQFADIIAMNADFIITSTYQEIAGSKNTV 493
QY 485 GQYESHTAFTPLGXYRVHGDIVDFPKFNIIVSGADMSIYFPHTEKAKRLTSLHGSINL 544
DB 494 GQYESHTAFTPLGXYRVHGDIVDFPKFNIIVSGADMSIYFPHTEKAKRLTSLHGSINL 553
QY 545 IYVPEQNDHEHGLDHSRKLPSMARLDVKNITGLVFAFAKCAKLELWNLVVVAGYN 604
DB 554 LFDPEQNDHEHGLDHSRKLPSMARLDVKNITGLVFAFAKCAKLELWNLVVVAGYN 613


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605 DVNKSXDRREIAEIEKMEHLEIKTNLFGQFRWISQNNRNARNGELIYRIADTHGAFVQPA 664
614 DVNKSXDRREIEIEKMEHLEIKTNLFGQFRWISQNNRNARNGELIYRIADTHGAFVQPA 673
665 LYEAAGLTUVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDPYHPEQAVNLMADFFORCK 724
674 FYEAAGLTUVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDPYHPEQAVNLMADFFORCK 733
725 QDPDHWNNISGAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 784
734 EDNHNKKVSDAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 793
785 LKFRDLAKTVPLAID 799
794 LKFRDLAKTVPESTAD 808

RESULT 6
Q9FRX3 PRELIMINARY; PRT; 812 AA.
AC Q9FRX3;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Sucrose synthase 1.
GN PYPSUS1.
OS Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Rosales; Rosaceae; Maloideae; Pyrus.
OX NCBI_TaxID=3767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Hosui; TISSUE=Fruit flesh;
RA Tanase K., Shiratake K., Mori H., Yamaki S.;
RT "Cloning and expression of SUS genes with development of Japanese pear
RT fruit.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045710; BAB20799.1; -.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco.trans.1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos.transf.1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 812 AA; 93079 MW; 8F9A26C08:E541B4 CRC64;

Query Match 80.5%; Score 3396; DB 10; Length 812;
Best Local Similarity 79.6%; Pred. No. 3.4e-242;
Matches 633; Conservative 84; Mismatches 76; Indels 2; Gaps 1;

7 DRVEDTLHARNELVALLSKYVKNKGILQPHHLDALDEVQ--SGGRALAEQPFLLDYL 64
15 ERVEDTLSDHRELVALLSRVLDQCKRIIQPHDLIDQLDVIIGVDBEAKQKQNGFFSEVL 74
65 RSAQAIIVLPPVAJAVRPPGVWEYVRVNVNHELVSVEQLTVSEYLRPKBELVDGQNDPY 124
75 KSAQAIIVLPPYVALAVRPPGVWDYVRVNVYELSVSEELTVSEYLRHFKBELVDGESSDKY 134
125 VLELDFEPFNVSVPNNSSSTGNGVOFLNRHLSSSTMPENRDLCLPDLFLGRHKGHV 184
135 VLELDFEPFNVAAPRPTSSSTGNGVOFLNRHLSSSTMPENRDLCLPDLFLGRHKGHV 194
185 MMLNDRIOSGLQSVLTAKAEHSLKLPADTPYSQFAYKFOEWGLEKMGWDTAGHYLEMI 244
135 LMLNDRIOSVSKLQALAKAEHSLKLPETYSSEYLFQKGFGRGWDTAHVLEMM 254
245 HLLLDIIQAPDPTLEKFLGRIPMIVNVVSVGHYFGQANVLGPDGTGGQIYVILDQVR 304
255 HLLLDIIQAPDPTLEKFLGRIPMIVNVVSVGHYFGQANVLGPDGTGGQIYVILDQVR 314
305 ALENEMVLEKQGLDVSFKIILVTLIPDAKGTSCNQLERISGQTHYTLIRVPRNEN 364

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315 ALEKMELEIRKQGLDTPRLLIVTRLIPEAKGITCNQLREISGTEHTHILRVPERSEK 374
365 GILKKWISRFDDVWPLETFAEDAAGEIAAELOQTGPDFIIGNYSDGNLVASLLSYKMGITQ 424
375 GILKKWISRFDDVWPLETFAEDAAGEIAAELOQTGPDFIIGNYSDGNLVASLLSYKMGITQ 434
425 CNIAHALEKTYPPDSIDFWKPNFDSKYHESCOPTADIIAMNADFIITSTYQBIAGSKNTV 484
435 CTIAHALEKTYPPDSIDFWKPNFDSKYHESCOPTADIIAMNADFIITSTYQBIAGSKNTV 494
485 QYESHSTAFTLPGLYRVVHGIDVDPKENIYVSPGADMSIYFPHTEKAKELTSLHSGIEML 544
495 QYESHSTAFTLPGLYRVVHGIDVDPKENIYVSPGADMSIYFPHTEKAKELTSLHSGIEML 554
545 IYDEQNDHEHGHLDLDRSKPILFEMARLORVKNITGLVEAFKAKAKELVNLVVAGVN 604
555 LYNPDQNDVHIGTILSDRSKPIIFSMARLDQVKNMTGLVEAFKAKAKELVNLVVAGVN 614
605 DVNKSXDRREIAEIEKMEHLEIKTNLFGQFRWISQNNRNARNGELIYRIADTHGAFVQPA 664
615 DVNKSXDRREIAEIEKMEHLEIKTNLFGQFRWISQNNRNARNGELIYRIADTHGAFVQPA 674
665 LYEAAGLTUVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDPYHPEQAVNLMADFFORCK 724
675 FYEAAGLTUVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDPYHPEQAVNLMADFFORCK 734
725 QDPDHWNNISGAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 784
735 EDPSYNNITISDAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 794
785 LKFRDLAKTVPLAID 799
795 LKFRDLAKTVPEAID 809

RESULT 7
Q84T18 PRELIMINARY; PRT; 811 AA.
AC Q84T18;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Sucrose synthase.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree;
RA Loureiro M., Kopka J., Mueller-Roeber B., Trethewey R.;
RT "Characterization of effects of specific reduction in gene expression
RT of two sucrose synthase genes in transgenic potato plants.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY205302; AAO67719.1; -.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco.trans.1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos.transf.1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 811 AA; 92775 MW; F4C99F1C862DD535 CRC64;

Query Match 80.1%; Score 3377; DB 10; Length 811;
Best Local Similarity 78.9%; Pred. No. 8.7e-241;
Matches 627; Conservative 84; Mismatches 82; Indels 2; Gaps 1;

7 DRVEDTLHARNELVALLSKYVKNKGILQPHHLDALDEV--QSGGRALAEQPFLLDYL 64
14 ERVEDTLHARNELVALLSKYVKNKGILQPHHLDALDEFNSAVCDTACEKLEKGGPFCEIL 73

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QY 65 RQAQAIULPPFAIAVAVRPPGVMEYVVRVNVHLSVEQLTVSEYLRKFEELVQGHNDPY 124
Db 74 KSTQEAIVLPPFAIAVAVRPPGVMEYVVRVNVHLSVEQLTVSEYLRKFEELVQGHNDPY 133
QY 125 VLELDFEPNPNVPPNRRSSISNGVQFLNRHLSSIMFRNDRCLPDLPLDFLRGHRKHGV 184
Db 134 VLELDFEPNPNVPPNRRSSISNGVQFLNRHLSSIMFRNDRCLPDLPLDFLRGHRKHGV 193
QY 185 MMLNDRIQSLRQSLVLTAEHLSKLDPADTPYSQAFYKQFQWGLKGWGDTAGHVLEMI 244
Db 194 LMLNERIQISRLSSINKADYLSKLPEPTPYTEPEYALQBMGFKGWGTAKRVLETM 253
QY 245 HLLLDIIQAPDSTLEKFLGRIPKIMENVVSVPHGVFGQANVLGLDTCGCIYVILDOVR 304
Db 254 HLLSDILOAPDSTLEKFLGRIPKIMENVVSVPHGVFGQANVLGLDTCGCIYVILDOVR 313
QY 305 ALNENMVLKKGGLDVSFKILVTLIPDAKTSQNRLEISGTHYVILRVPFRNEN 364
Db 314 ALNENMVLKKGGLDVSFKILVTLIPDAKTSQNRLEISGTHYVILRVPFRNEN 373
QY 365 GILKXWISRPDVPVYLETFAEDAAEIAELQGTDPFIIGNYSDGNLVASLLSYKMGITQ 424
Db 374 GILKXWISRPDVPVYLETFAEDAAEIAELQGTDPFIIGNYSDGNLVASLLSYKMGITQ 433
QY 425 CNIAHALEKTKYPSDSIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQELAGSKNTV 484
Db 434 CTIAHALEKTKYPSDSIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQELAGSKNTV 493
QY 485 GOYESHTAFTPLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPFTEKAKRLTSLHGSIEML 544
Db 494 GOYESHTAFTPLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPFTEKAKRLTSLHGSIEML 553
QY 545 IYDPEQNDHEHGLDSDRSKPIFSMARLDRVKNITGLVEAFKACAKRELNVLVVAGYN 604
Db 554 LEPDQNEVHIGNLQDSKPIFSMARLDRVKNITGLVEAFKACAKRELNVLVVAGYN 613
QY 605 DVNKSQDREIEAETKMKHELIKTNLFQGFRIWISAOQNRARNGELYRIADTHGAFVQPA 664
Db 614 DVNKSQDREIEAETKMKHELIKTNLFQGFRIWISAOQNRARNGELYRIADTHGAFVQPA 673
QY 665 LYAFGLTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHDIPYHPEQAVNLMAFFDRCK 724
Db 674 FYAFGLTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHDIPYHPEQAVNLMAFFDRCK 733
QY 725 QDPDHWNISAGLQRIYKTYKTIYKISERLMTAGVYGFNFKYVSKLELETRRYLEMYI 784
Db 734 QNP7HWNISAGLQRIYKTYKTIYKISERLMTAGVYGFNFKYVSKLELETRRYLEMYI 793
QY 785 LKFEELAKTVPLAID 799
Db 794 LKFEELAKTVPLAID 808

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RESULT 8

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Q9SBD5 ID Q9SBD5 PRELIMINARY; PRT; 808 AA.
AC Q9SBD5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE T2H3.8 protein.
GN T2H3.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_taxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA WastU;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Kallio J., Gibson A.;
RT "The sequence of A. thaliana T2H3.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075597; AAC28175.1; -.
DR PIR; T01420; T01420.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycosyl transferase 1; 1.
DR Pfam; PF00862; Sucrose synth. 1.
SQ SEQUENCE 808 AA; 92201 MW; DA32BF19005863BC CRC64;

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Query Match 79.8%; Score 3366; DB 10; Length 808;
 Best Local Similarity 78.9%; Pred. No. 5.6e-240;
 Matches 620; Conservative 88; Mismatches 64; Indels 14; Gaps 2;

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QY 7 DRYEDTLHAHRELVALLSKYVKNKGKILQPHHLDALDEVQSG--GRAEAGFFLDVL 64
Db 14 DRYQDTLSAHRNELVALLSRYVQKGLQPHNLIDELESVIGDDETKKSLSDGFFGEIL 73
QY 65 RSAQEAIVLPPFAIAVAVRPPGVMEYVVRVNVHLSVEQLTVSEYLRKFEELVQGHNDPY 124
Db 74 KSAMEALVPPFAIAVAVRPPGVMEYVVRVNVHLSVEQLTVSEYLRKFEELVQGHNDPY 133
QY 125 VLELDFEPNPNVPPNRRSSISNGVQFLNRHLSSIMFRNDRCLPDLPLDFLRGHRKHGV 184
Db 134 CLELDFEPNPNVPPNRRSSISNGVQFLNRHLSSIMFRNDRCLPDLPLDFLRGHRKHGV 193
QY 185 MMLNDRIQSLRQSLVLTAEHLSKLDPADTPYSQAFYKQFQWGLKGWGDTAGHVLEMI 244
Db 194 LMLNDRIQSLRQSLVLTAEHLSKLDPADTPYSQAFYKQFQWGLKGWGDTAGHVLEMI 253
QY 245 HLLLDIIQAPDSTLEKFLGRIPKIMENVVSVPHGVFGQANVLGLDTCGCIYVILDOVR 304
Db 254 HLLSDILOAPDSTLEKFLGRIPKIMENVVSVPHGVFGQANVLGLDTCGCIYVILDOVR 313
QY 305 ALNENMVLKKGGLDVSFKILVTLIPDAKTSQNRLEISGTHYVILRVPFRNEN 364
Db 314 ALNENMVLKKGGLDVSFKILVTLIPDAKTSQNRLEISGTHYVILRVPFRNEN 361
QY 365 GILKXWISRPDVPVYLETFAEDAAEIAELQGTDPFIIGNYSDGNLVASLLSYKMGITQ 424
Db 362 GILKXWISRPDVPVYLETFAEDAAEIAELQGTDPFIIGNYSDGNLVASLLMAHRMGVTQ 421
QY 425 CNIAHALEKTKYPSDSIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQELAGSKNTV 484
Db 422 CTIAHALEKTKYPSDSIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQELAGSKNTV 481
QY 485 GOYESHTAFTPLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPFTEKAKRLTSLHGSIEML 544
Db 482 GOYESHTAFTPLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPFTEKAKRLTSLHGSIEML 541
QY 545 IYDPEQNDHEHGLDSDRSKPIFSMARLDRVKNITGLVEAFKACAKRELNVLVVAGYN 604
Db 542 IYDPEQNDHEHGLDSDRSKPIFSMARLDRVKNITGLVEAFKACAKRELNVLVVAGYN 601
QY 605 DVNKSQDREIEAETKMKHELIKTNLFQGFRIWISAOQNRARNGELYRIADTHGAFVQPA 664
Db 602 DVNKSQDREIEAETKMKHELIKTNLFQGFRIWISAOQNRARNGELYRIADTHGAFVQPA 661
QY 665 LYAFGLTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHDIPYHPEQAVNLMAFFDRCK 724
Db 662 FYAFGLTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHDIPYHPEQAVNLMAFFDRCK 721

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QY 125 VLELDFEPFNVPNRPNSSSIGNGVQFLNRHLSSIMFRNDCLEPLDPLFGRHRKHGV 184
 Db 134 VLELDFEPFNVPNRPNSSSIGNGVQFLNRHLSSIMFRNDCLEPLDPLFGRHRKHGV 193
 QY 185 MMLNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQPAYKFOEWGLEKMGCDTAGHLEMI 244
 Db 194 MMLNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQPAYKFOEWGLEKMGCDTAGHLEMI 253
 QY 245 HLLLDIIQADPSTLEKFLGRIPMIPNVVWVPHGVFGQANVLGLDPTGGQIVYLQV 304
 Db 254 HLLSDILQADPSTLEKFLGRIPMIPNVVWVPHGVFGQANVLGLDPTGGQIVYLQV 313
 QY 305 ALNEMVRLKXGDLVSPKILVTRLIPDAKGTSCNQLERISGTHYILRVPPREN 364
 Db 314 ALNEMVRLKXGDLVSPKILVTRLIPDAKGTSCNQLERISGTHYILRVPPREN 373
 QY 365 GILKWKISFDWPNY-ETFAEDAAGEIAELQCTPDIIGNTSDGNLVSLLSYKMGITQ 424
 Db 374 GILKWKISFDWPNY-ETFAEDAAGEIAELQCTPDIIGNTSDGNLVSLLSYKMGITQ 433
 QY 425 CNIAHALEKTKYDSDIFWKNDEKHFSCQFTADIIAMNADFLITSTYQETAGSKNTV 484
 Db 434 CNIAHALEKTKYDSDIFWKNDEKHFSCQFTADIIAMNADFLITSTYQETAGSKNTV 493
 QY 485 GOYESHATPLGLYRVVHGIDVDFPKFNIVSPGADMSYFPHTKAKRLTSLHGSIEML 544
 Db 494 GOYESHATPLGLYRVVHGIDVDFPKFNIVSPGADMSYFPHTKAKRLTSLHGSIEML 553
 QY 545 IYDPEONDEHIGLDRSKPILFPMARLDRVKNITGLVEAFACAKLRELNLVWVAGYN 604
 Db 554 IYDPEONDEHIGLDRSKPILFPMARLDRVKNITGLVEAFACAKLRELNLVWVAGYN 613
 QY 605 DVNKSXDREIEAIEKXHELIKTHNLFGQPRWISAGTNRARNGELRYIADTHGAFVQPA 664
 Db 614 DVNKSXDREIEAIEKXHELIKTHNLFGQPRWISAGTNRARNGELRYIADTHGAFVQPA 673
 QY 665 LYFAFGLTVVEAMTCGLPTATLGGPAEIIHGVSGFHDIDPHBQAVNLMAADFFDRCK 724
 Db 674 LYFAFGLTVVEAMTCGLPTATLGGPAEIIHGVSGFHDIDPHBQAVNLMAADFFDRCK 733
 QY 725 QDPDHWNVISGAGLQRIYKTYWKIYSERLMTLAGVVGFWKYVSKLERLETRRYLEMYI 784
 Db 734 QDPDHWNVISGAGLQRIYKTYWKIYSERLMTLAGVVGFWKYVSKLERLETRRYLEMYI 793
 QY 785 LKPRELAKTVPLAID 799
 Db 794 LKPRELAKTVPLAID 808

RESULT 11
 Q92PC6 PRELIMINARY; PRT; 809 AA.
 ID Q92PC6
 AC Q92PC6
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sucrose synthase [SC 2.4.1.13].
 GN SS1.
 OS Craterostigma plantagineum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Craterostigma plantagineum.
 OC NCBI_TaxID=4153;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=39396657; PubMed=10467027;
 RA Kleines M., Elster R.C., Rodrigo M.J., Blervacq A.S., Salami F.,
 RA Bartels D.;
 RT "Isolation and expression analysis of two stress-responsive sucrose-
 RT synthase genes from the resurrection plant Craterostigma plantagineum
 RT (Hochst.)";
 RL Planta 209:13-24(1999).

DR EXBL, AJ131999; CAB38021.1; -;
 DR GO:0016157; F:sucrose synthase activity; IEA.
 DR GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
 DR GO:0009058; P:biocatalysis; IEA.
 DR GO:0005985; P:sucrose metabolism; IEA.
 DR InterPro:IPR001296; Glyco trans 1.
 DR InterPro:IPR00368; Sucrose synth.
 DR Pfam:PF00534; Glyco_transf_1; 1.
 DR Pfam:PF00862; Sucrose synth; 1.
 DR Glycosyltransferase; Transferase.
 KW GLYCOSYLTRANSFERASE; TRANSFERASE;
 SQ SEQUENCE 809 AA; 92663 MW; 9CC752AEC739AFE0 CRC64;

Query Match 73.9%; Score 3117; DB 10; Length 809;
 Best Local Similarity 73.3%; Pred. No. 15e-221;
 Matches 593; Conservative 92; Mismatches 118; Indels 2; Gaps 1;

QY 7 DRVEDTJAHRNELVALLSKYVNGKGILOPHHILDALDE--VOGSGRALAAGPFLDVL 64
 Db 15 ERVEETADHROELISLLSKYTSRGKCLQSHQMDLEDAIAEDPANKKLSGCGFNEVL 74
 QY 65 RSAQEAIVLPFPVATIAVRPRPGWVYRVNVVHLSVEQLTVSEYLFKEELVDGQNDPY 124
 Db 75 SSAQEAIVLPFPVATIAVRPRPGWVYRVNVVHLSVEQLTVSEYLFKEELVDGQNDPY 134
 QY 125 VLELDFEPFNVPNRPNSSSIGNGVQFLNRHLSSIMFRNDCLEPLDPLFGRHRKHGV 184
 Db 135 VLELDFEPFNVPNRPNSSSIGNGVQFLNRHLSSIMFRNDCLEPLDPLFGRHRKHGV 194
 QY 185 MMLNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQPAYKFOEWGLEKMGCDTAGHLEMI 244
 Db 195 MMLNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQPAYKFOEWGLEKMGCDTAGHLEMI 254
 QY 245 HLLLDIIQADPSTLEKFLGRIPMIPNVVWVPHGVFGQANVLGLDPTGGQIVYLQV 304
 Db 255 HLLSDILQADPSTLEKFLGRIPMIPNVVWVPHGVFGQANVLGLDPTGGQIVYLQV 314
 QY 305 ALNEMVRLKXGDLVSPKILVTRLIPDAKGTSCNQLERISGTHYILRVPPREN 364
 Db 315 ALNEMVRLKXGDLVSPKILVTRLIPDAKGTSCNQLERISGTHYILRVPPREN 374
 QY 365 GILKWKISFDWPNY-ETFAEDAAGEIAELQCTPDIIGNTSDGNLVSLLSYKMGITQ 424
 Db 375 GILKWKISFDWPNY-ETFAEDAAGEIAELQCTPDIIGNTSDGNLVSLLSYKMGITQ 434
 QY 425 CNIAHALEKTKYDSDIFWKNDEKHFSCQFTADIIAMNADFLITSTYQETAGSKNTV 484
 Db 435 CNIAHALEKTKYDSDIFWKNDEKHFSCQFTADIIAMNADFLITSTYQETAGSKNTV 494
 QY 485 GOYESHATPLGLYRVVHGIDVDFPKFNIVSPGADMSYFPHTKAKRLTSLHGSIEML 544
 Db 495 GOYESHATPLGLYRVVHGIDVDFPKFNIVSPGADMSYFPHTKAKRLTSLHGSIEML 554
 QY 545 IYDPEONDEHIGLDRSKPILFPMARLDRVKNITGLVEAFACAKLRELNLVWVAGYN 604
 Db 555 IYDPEONDEHIGLDRSKPILFPMARLDRVKNITGLVEAFACAKLRELNLVWVAGYN 614
 QY 605 DVNKSXDREIEAIEKXHELIKTHNLFGQPRWISAGTNRARNGELRYIADTHGAFVQPA 664
 Db 615 DVNKSXDREIEAIEKXHELIKTHNLFGQPRWISAGTNRARNGELRYIADTHGAFVQPA 674
 QY 665 LYFAFGLTVVEAMTCGLPTATLGGPAEIIHGVSGFHDIDPHBQAVNLMAADFFDRCK 724
 Db 675 LYFAFGLTVVEAMTCGLPTATLGGPAEIIHGVSGFHDIDPHBQAVNLMAADFFDRCK 734
 QY 725 QDPDHWNVISGAGLQRIYKTYWKIYSERLMTLAGVVGFWKYVSKLERLETRRYLEMYI 784
 Db 735 QDPDHWNVISGAGLQRIYKTYWKIYSERLMTLAGVVGFWKYVSKLERLETRRYLEMYI 794
 QY 785 LKPRELAKTVPLAID 799
 Db 795 LKPRELAKTVPLAID 809

RESULT 12

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Q9SBL8      PRELIMINARY;      PRT;      806 AA.
ID          AC          Q9SBL8;
AC          DT          01-MAY-2000 (T-EMBLrel. 13, Created)
DT          DT          01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT          DT          01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE          DE          WSUS.
GN          OS          Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OS          OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC          OC          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC          OC          eurosid2; Cucurbitales; Cucurbitaceae; Citrullus.
OX          NCB1_TaxID=3654;
RN          RP          SEQUENCE FROM N.A.
RA          RA          Kim J., Kang H., Jun S., Lee J., An G.;
RT          RT          "Watermelon mRNA for GA3-regulated in developing seeds, complete cds.
RT          RT          (Cloning of three gibberellin-regulated cDNAs from watermelon during
RT          RT          early seed development: down-regulated one cDNA and up-regulated two
RT          RT          cDNAs).";
RL          RL          Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR          DR          EMBL; AB018561; BAA89232.1; -.
DR          GO; GO:0009058; P:biosynthesis; IEA.
DR          GO; GO:0005985; P:sucrose metabolism; IEA.
DR          InterPro; IPR001296; Glyco_trans_1.
DR          InterPro; IPR000368; Sucrose synth.
DR          Pfam; PF00534; Glycos transf_1; 1.
DR          Pfam; PF00862; Sucrose synth; 1.
SQ          SEQUENCE      806 AA; 92559 MW; 4FD8ECAD6C140337 CRC64;

Query Match      71.1%; Score 2998.5; DB 10; Length 806;
Best Local Similarity      70.2%; Pred. No. 8.7e-213;
Matches 560; Conservative 111; Mismatches 126; Indels 1; Gaps 1;

QY      3 HASDRVEDTLHAHRELVALLSKVYKNGKGILOPHHILDALDEWQSGGRALAEGLD 62
DB      10 HSRERIGDSLSAHPNELVAVFTRLVNIGKQKLOPHQIIAEYNNNAIPEARD---KLKDG 70
QY      63 VLRSQAQAIVLPPFVALAIVPRPGVWYVYRVNVHLSVEQITVSEYLFKBEELVDG 122
DB      70 VLRTQESIVLPPFVALAIVPRPGVWYVYRVNVHLSVEQITVSEYLFKBEELVDG 129
QY      123 PYVLELDFEFPNVSPPRNPSSSGTNGVQFLNRHLSIMFNRDCLDPLDLRGHREK 182
DB      130 NFVLELDFEFPNASFPRTT-SKSTGNGVFEFLNRHLSAKLPHGKESMQPLDLFLRVHCYK 189
QY      183 HVMMNDRIQSLGRQSLTKAESHLSKLPADTPYSQFAYKFBQWGLEKMGDTAGHVLE 242
DB      190 KTMNDRIQTLNFAQVLRKAESYLATLAPETPYSSEFANKFEIIGLERGWNTERVLE 249
QY      243 MIHLLDIIQAPDPTLEKFLGRIPMIFFNVVSPHGVFGQANVLGLPDTGGQIVYILDQ 302
DB      250 MIQLLLEAPDPTCEKFLGRIPMVFNVILSPHGVFGQANVLGLPDTGGQIVYILDQ 309
QY      303 VRALENEMVLKQGLDVSFKIIVTRLIIPDAKGTSCNQLERISGTHYILRV 362
DB      310 VRALEHEMLQSIKQGLDITPRILIIITRLDPDVGTTCTQBLEKVFGEHSHILRV 369
QY      363 ENGLIKWISFDVWPVLETAEDAAGBIAELOQTDPFIIGNYSDGNLVSILSYKMG 422
DB      370 EKGIVRWKISFVWPVLETTEDVAQBLTKELQKPDILLIGNYSDGNLVSILAHKLV 429
QY      423 TQCNIAHALEKTKYPCSDIFWKNFDEKVFSCQFTADIIAMNADFIITSTYQEIAGSK 482
DB      430 TQCTIAHALEKTKYPCSDIYKRDYKXFFSQFTADLIAMNHTDFTITSTFQEIAGSK 489
QY      483 TVGOYESHATPLCLTRVWIGIDVDFPKFNVISPGADMSYFFHTEKAKDLTSLGSI 542
DB      490 TVGOYESHATPLCLTRVWIGIDVDFPKFNVISPGADMSYFFHTEKAKDLTSLGSI 549
QY      543 NLIYDPEQNDHGHLLDDRSKPIILFMSMARLDVRKNITGLVEYFAFKAKLRELNVLVVAG 602
DB      544 NLIYDPEQNDHGHLLDDRSKPIILFMSMARLDVRKNITGLVEYFAFKAKLRELNVLVVAG 602

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DB      550 ELLYSEVENEHLVCLDRSKPIIFTMARLDVRKNITGLVEYKGNKRLRELNVLVVAG 609
QY      603 YNDVNSKDRBETAEIKMEHLIKTNLFCQFRMISQATPRANGELYRYIADTHGAFVQ 662
DB      610 -DRRKESKDNEEKAEKEMKYLITKYNLNGQFRMISQATPRANGELYRYIADTHGAFVQ 668
QY      663 PALYEAFLGVTWAMTCTCLPTFATLHGGPABIIIEHGVSGPHIDIPHPQAVNLMAFDPR 722
DB      669 PAVYEAFLGVTWAMTCTCLPTFATLHGGPABIIIEHGVSGPHIDIPHPQAVNLMAFDPR 728
QY      723 CKQDPDHWNVISGAGLQRIYKTYTWKISYERIMTLGAVYGVKVKYVKLERLETRYLEMP 782
DB      729 SKEDPSHWKISQAGLQRIYKTYTWKISYERIMTLGAVYGVKVKYVKLERLETRYLEMP 788
QY      783 YILKRELAKTVPLAIDQ 800
DB      789 YALKYRKLADSVPOAVDE 806

RESULT 13
Q8WIM4      PRELIMINARY;      PRT;      816 AA.
ID          AC          Q8WIM4;
AC          DT          01-MAR-2002 (T-EMBLrel. 20, Created)
DT          DT          01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT          DT          01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE          DE          Sucrose synthase 2.
OS          OS          Bambusa oldhamii (Giant timber bamboo).
OC          OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC          OC          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC          OC          Bambusoideae; Bambuseae; Bambusa.
OX          NCB1_TaxID=56923;
RN          RP          SEQUENCE FROM N.A.
RA          RA          Lin C.-H., Wang A.-Y.;
RT          RT          "Sucrose synthase in green bamboo Bambusa oldhamii.";
RT          RT          Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AF412037; AAL50570.1; -.
DR          GO; GO:0009058; P:biosynthesis; IEA.
DR          GO; GO:0005985; P:sucrose metabolism; IEA.
DR          InterPro; IPR001296; Glyco_trans_1.
DR          InterPro; IPR000368; Sucrose synth.
DR          Pfam; PF00534; Glycos transf_1; 1.
DR          Pfam; PF00862; Sucrose synth; 1.
SQ          SEQUENCE      816 AA; 92361 MW; EF4067896E51020D CRC64;

Query Match      70.9%; Score 2991; DB 10; Length 816;
Best Local Similarity      69.8%; Pred. No. 3.2e-212;
Matches 559; Conservative 108; Mismatches 126; Indels 8; Gaps 3;

QY      3 HASDRVEDTLHAHRELVALLSKVYKNGKGILOPHHIL---DALDEWQSGGRALAE 58
DB      14 HSRERIGDSLSAHPNELVAVFTRLVNIGKQKLOPHQIIAEYNNNAIPEARD---KLKDG 70
QY      59 PFLDVLRSQAQAIVLPPFVALAIVPRPGVWYVYRVNVHLSVEQITVSEYLFKBEELVD 118
DB      71 AFEDVLRAQAIVLPPFVALAIVPRPGVWYVYRVNVHLSVEQITVSEYLFKBEELVD 130
QY      119 QHNDPYVLELDFEFPNVSPPRNPSSSGTNGVQFLNRHLSIMFNRDCLDPLDLRGH 178
DB      131 STNNFVLELDFEFPNASFPRTT-SKSTGNGVFEFLNRHLSAKLPHGKESMQPLDLFLRV 190
QY      179 RHKGHVMMNDRIQSLGRQSLTKAESHLSKLPADTPYSQFAYKFBQWGLEKMGDTAG 238
DB      191 NYKGMTMNDRIQSLGRQSLTKAESHLSKLPADTPYSQFAYKFBQWGLEKMGDTAG 250
QY      239 HVLEMIHLLDIIQAPDPTLEKFLGRIPMIFFNVVSPHGVFGQANVLGLPDTGGQIVY 298
DB      251 RAQETIHLLEAPDPTCEKFLGRIPMVFNVILSPHGVFGQANVLGLPDTGGQIVY 310
QY      299 ILDOVRALENEMVLKQGLDVSFKIIVTRLIIPDAKGTSCNQLERISGTHYILRV 358
DB      311 ILDOVRALENEMVLKQGLDVSFKIIVTRLIIPDAKGTSCNQLERISGTHYILRV 370

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Qy	359	PPRNGILKKWISRFDPVWPYLETFAEDAAGEIAAEALQGTDPFIIGNYSQGNLVASLSY	418
Db	371	PPRNGILKKWISRFDPVWPYLETFAEDAAGEIAAEALQGTDPFIIGNYSQGNLVASLSY	430
Qy	419	KMGICQCNIAHALEKTKYPSDSIFWNFDEKXHFSCQFTADIAMNADFIITSTYOBIA	478
Db	431	KMGVTHCTIAHALEKTKYPSDSIFWNFDEKXHFSCQFTADIAMNADFIITSTYOBIA	490
Qy	479	GSKNTVGVESHATLPLGLRVVHGIDVDFPKENIVSPGADMSIYFFPHTEKAKLTSLH	538
Db	491	GKNDTVGVESHATLPLGLRVVHGIDVDFPKENIVSPGADMSIYFFPHTEKAKLTSLH	550
Qy	539	GSIEMLIYDPEONDEHIGLDRSKPILFSPMARLDVRKNITGLVEFAFAKAKLRELNVIV	598
Db	551	PIEIELLYSDVDNNEKFLVLDKRNKPIIFSPMARLDVRKNITGLVEFAFAKAKLRELNVIV	610
Qy	599	VWAGYNDVNSKDRERIEAIEKMHILKTHNLFCQFRWISAOQNRNARNGELYRIADTHG	658
Db	611	VWCG-DHGNPSKDEQAEFKMFHIEQNLNGHRIWISAOQNRNARNGELYRIADTHG	669
Qy	659	AFVQALYEAFLGTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHDIDPYHPQAVNLMD	718
Db	670	AFVQALYEAFLGTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHDIDPYHPQAVNLMD	729
Qy	719	FFDRCKQDPHWNISGAGLQRIYEKYTWKIYSERLMTAGVYGVFWKYVSKLERLTRY	778
Db	730	FFDRCKQDPHWNISGAGLQRIYEKYTWKIYSERLMTAGVYGVFWKYVSKLERLTRY	789
Qy	779	LEMFYIKRELAKTVPLAID 799	
Db	790	LEMFYIKRELAKTVPLAID 810	
RESULT 14			
ID	Q9SL52	PRELIMINARY; PRT; 805 AA.	
AC	Q9SL52		
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)		
DE	Sucrose synthase.		
GN	CITSUS1-2.		
OS	Citrus unshiu (Satsuma orange).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Sapindales; Rutaceae; Citrus.		
OX	NCBI_TaxID=55188;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Miyagawa-wase;		
RA	Komatsu A.;		
RT	"Cloning of sucrose synthase (CITSUS1) gene from Citrus.";		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB29401; BAB89049.1; -		
DR	GO; GO:0005958; P:biogenesis; IEA.		
DR	GO; GO:0005985; P:sucrose metabolism; IEA.		
DR	InterPro; IPR001296; Glyco trans 1.		
DR	InterPro; IPR000368; Sucrose synth.		
DR	Pfam; PF00534; Glycosylase 1.		
DR	Pfam; PF00862; Sucrose synth 1.		
SQ	SEQUENCE 805 AA; 92172 MW; 2098FCLF524C266E CRC64;		
Query Match			
Best Local Similarity 69.6%; Pred. NO. 9.4e-212;			
Matches 555; Conservative 115; Mismatches 126; Indels 1; Gaps 1;			
Qy	3	HASGRVEDTLAHNELVALLSKYVNGKGILOPHHILDALDEVOSSGGRALAGPPLD	62
Db	10	HSLRLEJDETLSAHRNETALLSRIEGKGILOPHHILDALDEVOSSGGRALAGPPLD	69
Qy	63	VLSAQEAIVLPPFVAJAVRPPGVWVYRVNVHLSVEQLTVSVLYLFFKEELVDGQND	122
Db	63	VLSAQEAIVLPPFVAJAVRPPGVWVYRVNVHLSVEQLTVSVLYLFFKEELVDGQND	122
RESULT 15			
ID	Q8W1W3	PRELIMINARY; PRT; 808 AA.	
AC	Q8W1W3		
DT	01-MAR-2002 (TREMBlrel. 20, Created)		
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)		
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)		
DE	Sucrose synthase 1.		
OS	Bambusa oldhamii (Giant timber bamboo).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Bambusoideae; Bambuseae; Bambusa.		
OX	NCBI_TaxID=58923;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lin C.-H., Wang A.-Y.;		
RT	"Sucrose synthase in green bamboo Bambusa oldhamii.";		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF412038; AAL50571.1; -		
DR	GO; GO:0005988; P:biogenesis; IEA.		
DR	GO; GO:0005985; P:sucrose metabolism; IEA.		
DR	InterPro; IPR001296; Glyco trans 1.		

DR	InterPro: IPR000363; Sucrose synth.									
DR	Pfam: PF00534; Glycos transf 1; 1.									
DR	Pfam: PF00862; Sucrose synth; 1.									
SQ	SEQUENCE 808 AA; 92252 MW; C5C0B5C67A58F518 CRC64;									
Query Match 70.7%; Score 2982.5; DB 10; Length 808;										
Best Local Similarity 69.8%; Pred. No. 1.3e-211;										
Matches 556; Conservative 103; Mismatches 135; Indels 3; Gaps 2;										
QY	3	HASGRVEDTLHAHRELVELVALLSKYVKNKGILQPHHILDALDEVQSGGRALAEAGPFLD	62							
DB	9	HSURERUSATFSSHPNELIALFSRYVHQKQKMLQRHQLIAEFDALIAADKEKYA--PFED	66							
QY	63	VLSAQEAIVLPFVALAIVPRGVMEYRVNVVHLSVQLTVSEYLRKFEELVDGQND	122							
DB	67	ILRAAQEAIVLPWVALAIVPRGVWDYIRNVSELAVEELSVESEYLFKEQLVDGHTNS	126							
QY	123	PVULELDFEPNVSVPRPNRSSISGNGVQFLNRHLSIMFRNRDCLEPLDLFLGRHRHG	182							
DB	127	NFVLELDFEPFNASFRPMSKSGNGVQFLNRHLSKLFQDKESLYPLNLFKAHMHG	186							
QY	183	HVMMLNDRIQSLGRQSLVTKAEHLKSLPADTPYQFAFKQFQEWGLEKQWGTAGHYLE	242							
DB	187	TTMMLNDRIQSLGRQSLAKABEYLMSPQDTPYSEFNRFQELGLEKQWGTAKRVL	246							
QY	243	MIHLILDIICAPDSLEKELGRIPMTFNVVVSPHGYFGQANVLGLPDTGCGIIVYILDQ	302							
DB	247	TIHLDDLLEAPDPANLEKFLGTPMTFNVVILSPHGYFAQSNVLGYPTDGGQVYILDQ	306							
QY	303	VRALENEMLRKQGLDVPKILIVTRLPDAKGTSCNQRLEKISGTOHTYILRVFPRN	362							
DB	307	VRALENEMLRKQGLDVPKILIVTRLPDAKGTTCGQLEKVICGUEHTDILRVFPRT	366							
QY	363	ENGLKRWISRFQWVPLETFAEDAAEIAELQGTDFIIGNYSDGNLVASLLSYKGI	422							
DB	367	ENGLKRWISRFQWVPLETFAEDAAEIAELQGTDFIIGNYSDGNLVATLIAHLGV	426							
QY	423	TQCTIAHALEKTYPPDSDIWKNFDEKHYFSCQFTADIAMNNADFIITSTYQRIAGSKN	482							
DB	427	TQCTIAHALEKTYPPDSDIWKNFDEKHYFSCQFTADLIAMNHTDFIITSTYQRIAGSKD	486							
QY	483	TVGQYESHATAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE	542							
DB	487	TVGQYESHATAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE	546							
QY	543	NLIYDPEQNDHGHLDLDRKPIFLFSMARLDVRKNIITGLVEAFKAKRLRELVLVYVAG	602							
DB	547	ELLYSDVENSEHKEFVKDKNKPILIFSARLDVRKNIITGLVEAFKAKRLRELVLVYVAG	606							
QY	603	YNDVNSKDRREIAEIEKHMLIKTHLFGQFMTISACTNEARNGELRYRIADTHGAFVQ	662							
DB	607	-DHGKSKDRREIAEIEKHMLIKTHLFGQFMTISACTNEARNGELRYRIADTHGAFVQ	665							
QY	663	PALYEAFLGTIVVEAMTCLPTFATLHGQPAEIIIEHGVSGFHDIPYHPPEQAVNLMAFPDR	722							
DB	666	PAFYEAFLGTIVESMTCLPTIATCHGQPAEIIIVDGVSGLIHDPVHSNKAADILVNPFEK	725							
QY	723	CKQDPDHWNITSGAGLQRIYKTYWKIYSERLMILAGVYGFVKYVSKLERLETRRYLEMP	782							
DB	726	CKEDPTWMDKISQGLKRIYKTYWKIYSERLMILAGVYGFVKYVSKLERLETRRYLEMP	785							
QY	783	YILKFERELAKTVPLAID	799							
DB	786	YALKYRSLASAVPLAID	802							

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 17.424 Seconds
(without alignments)
4427.559 Million cell updates/sec

Title: US-10-080-114a-2

Perfect score: 4217

Sequence: 1 STHASGRVEDTLAHRNEL.....YILKRELAKTVPLAIDQPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Length	DB ID	Description
1	3456	82.0	809	2 B85029	probable sucrose s
2	3397.5	80.6	809	2 T06497	probable sucrose s
3	3366	79.8	808	2 T01420	sucrose synthase
4	3302	78.3	822	2 S71493	sucrose synthase
5	3045	72.2	804	1 YUMU	sucrose synthase
6	2993.5	71.0	802	1 YUZMS	sucrose synthase
7	2990.5	70.9	808	2 S23543	sucrose synthase
8	2965	70.3	816	2 S19139	sucrose synthase
9	2944.5	69.8	805	1 YUPOS	sucrose synthase
10	2944.5	69.8	806	2 S31479	sucrose synthase
11	2922	69.3	816	2 S32451	sucrose synthase
12	2910.5	69.0	808	2 S73560	sucrose synthase
13	2904.5	68.9	808	2 T49233	sucrose synthase-1
14	2899	68.7	807	2 S29242	sucrose synthase
15	2861.5	67.9	801	2 T14338	sucrose synthase
16	2340.5	55.5	942	2 C96762	probable sucrose s
17	2259.5	53.6	586	2 S24966	sucrose synthase
18	1833	43.5	906	2 A12428	sucrose synthase
19	1506	35.7	805	2 AH1938	sucrose synthase
20	843.5	20.0	235	2 J10281	sucrose synthase
21	778.5	18.5	212	2 JT0280	sucrose synthase
22	739	17.5	204	2 S22535	sucrose synthase
23	681.5	16.2	179	2 S22537	sucrose synthase
24	587.5	13.9	218	2 S22131	sucrose synthase
25	515	12.2	127	2 A29484	sucrose synthase
26	467.5	11.1	720	2 S75935	hypothetical prote
27	466.5	11.1	1083	2 T04062	sucrose-phosphate
28	450	10.7	1056	2 JQ2277	sucrose-phosphate
29	445	10.6	1059	2 T12195	sucrose-phosphate

ALIGNMENTS

RESULT 1

B85029

probable sucrose synthetase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001

C:Accession: B85029

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: B85029

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-809 <STO>

A:Cross-references: GB_NC_001268; NID:g7268989; PIDN:CAB80721.1; GSPDB:GM00140

C:Genetics:

A:Gene: AT4G02280

A:Map position: 4

C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

Query Match	82.0%	Score	3456	DB 2	Length	809
Best Local Similarity	79.9%	Pred. No.	3	8e-223		
Matches	635	Conservative	89	Mismatches	69	Indels
						Gaps
QY	7	DRVEDTLAHRNELVALLSKYKNGKILQPHHLDALDEVQSG--GRALAEQPFDLVL	64			
Db	14	DRVQDTLSAHRNELVALLSRVYDQKGKILQPHNLIDELSVICDDTKKSLSDGPFGEIL	73			
QY	65	RSQAQAVILPPFAVAVRPGVWEYRVNVVHLSVQLTVSEYLRFKELVDGQHNDPY	124			
Db	74	KSAMEAVVPPFVALAVRPGVWEYRVNVVHLSVQLTVSEYLRFKELVDGQNSDPF	133			
QY	125	VLEDFEFPNVSPRPNRSSISGNGVQFLNRHLSSIMERNRDLCEPLDLFLGRHKGHV	184			
Db	134	CLELDFEFPNVANVPSPRSSISGNGVQFLNRHLSSIMERNRDLCEPLDLFLRVHKGHP	193			
QY	185	MLMDRIQSLGRQLSVLTKAEHLKSLPADTYPQYKQFQWGLEKKGWDGTAHVLEMI	244			
Db	194	LMMDRIQSLQSLQSLKAEDHISKLSQETPFSEFVALQGMGFEKMGWDGTAHVLEMM	253			
QY	245	HLILLIQAPDPSSTLEKFLGRIPMIVNVVSPHGVGOANVLGLPDTGQIVYLLDOVR	304			
Db	254	HLLSILOAPDPSSTLEKFLGMVPMVNVVILSPHGVGOANVLGLPDTGQIVYLLDOVR	313			
QY	305	ALENEMWLKKGDLVSPKILIVTRLPDAKGTSCNQLERISGTQHTVYILRVPRNEN	364			
Db	314	ALETMLKIKKGDLVSPKILIVTRLPDAKGTSCNQLERISGTQHTVYILRVPRNEN	373			
QY	365	GILKWKISFDWPPYLETFAEDAAGSIAAELOCTDPTFIIGNYSDGNLVASLSYKNGITQ	424			
Db	374	GILKWKISFDWPPYLETFAEDAAGSIAAELOCTDPTFIIGNYSDGNLVASLSYKNGITQ	433			

425 QY CNIAHALEKTYKPPSDIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQFIAGSKNTV 484
434 DB CTIAHALEKTYKPPSDIYWKDFDNKYHFSQFTADIIAONNADFIITSTYQFIAGTKNTV 493
485 QY GQYESHATAFTLPGYRVVHGIDVDPKNIYSPGADMSIYPPHTEKAKRLTSLHSGSIENL 544
494 DB GQYESHGTAFTLPGYRVVHGIDVDPKNIYSPGADMTIYPPSBETRLPALHSGSIEM 553
545 QY IYDPQNDHEHGLHDDRSKPIFLSMARLDVRVNIITGLVEAFKAKAKRELNLVNVVAGVN 604
554 DB LYSPTQDSHGVTLSDRSKPIFLSMARLDKVNISGLVEMYSKTKRELNLVVIAGNI 613
605 QY DVNKSQRREIABIEMHKLKTHNLFGQFRMISAGTRARNGELRYIADTHGAFVQPA 664
614 DB DVNKSQRREIABIEMHKLKTHNLFGQFRMISAGTRARNGELRYIADTHGAFVQPA 673
665 QY LYAEAGLTVEAMTCGLPTFATLHGCPAEIIEHGVSGPHIDPHYHPEQAVNLMAFFDRCK 724
674 DB FYAEAGLTVEAMTCGLPTFATLHGCPAEIIEHGVSGPHIDPHYHPEQAVNLMAFFDRCK 733
725 QY QCPDHVNVISAGLQRIYKYTWKIYSERLMTLAGYGVGWKVVSKLERLETRRYLEMFIY 784
734 DB EDENHWKXVSAGLQRIYKYTWKIYSERLMTLAGYGVGWKVVSKLERLETRRYLEMFIY 793
785 QY LKFRRELAKTVPLAID 799
794 DB LKFRDLVKTVPSTAD 808

RESULT 2
T06497
probable sucrose synthase (EC 2.4.1.13) 2 - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2003
C:Accession: T06497
R:Buchner, P.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z15720
A:Accession: T06497
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-809 <BUC>
A:Cross-references: EMBL:AJ001071; PIDN:CAA04512.1
A:Experimental source: cultivar Frisson
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:282-757/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 80.6%; Score 3397.5; DB 2; Length 809;
Best Local Similarity 78.9%; Pred. No. 3.1e-219; Indels 9; Gaps 2;
Matches 636; Conservative 80; Mismatches 81

QY 1 STE-----ASGDRVEDTIAHARNELVALLSKYVNGKGILOPHHILDALDEVQSGGR 53
DB 2 STHPKTRVPSIDRVQDTLSAARNELISLSRYVAQKGKILQPHNLIDELNDILGEDHA 61

QY 54 A--LAEGPFLDVLRSQAELVLPFVAIAVRPPGWYVYRVNVHLSVEQLTVSEYLR 111
DB 62 TLDLKNGPFQIINSAQEAIVLPFVAIAVRPPGWYVYRVNVHLSVEQLTVSEYLSF 121

QY 112 KEELVNGQNDPVLELDFEPNVSVPRNRSSIGNGVQFLNRHLSIMFRNRDCLLEPL 171
DB 122 KEELVEGSKNDNIIEULDELFNAPFRPRTRSSIGNGVQFLNRHLSIMFRNRDCLLEPL 181

QY 172 LDFLRGHRHKGHVMMMDRIQSLGRLOSILTKAEHLISKLPADTPYSQFYKQEWGLEK 231
DB 182 LDFLRVHTYKGHALMDRIQSLKQSLQALVKAEDHLSKLPADTPYSEFEYELQGTGER 241

QY 232 GWGDTAGHVLEMTHLLDITQADPSTLEKFLGRIPMFNVVVVSPKGYGQANVLGLPD 291
DB 242 GWGDTAARVLEMMHLLDILQADPSTLETFLGRVPVNVFNVLSPHGFQANVLGLPD 301

QY 292 TGSQIVVILDQVRALENMVLRLKKQGLDVSFKLIIIVTRLIPDAKGTSCNQLERISGTQ 351

302 DB TGGQVVVILDQVRALESEMLVRIKKQGLDFTPRILLIVTRLIPDAKGTTCNQLERVSGTE 361
352 QY HTYLILVRPFRBENGILKWIISDFVWPYLETFAEBAAGHIAELAQCTPDIIGNYSDGNL 411
362 DB YTHILVRPFRBENGILKWIISDFVWPYLETFAEBAAGHIAELAQCTPDIIGNYSDGNL 421
412 QY VASLLSYKMGITQCNIAHALEKTYKPPSDIFWKNFDEKHFSCQFTADIIAMNADFIIT 471
422 DB VASLLAYKMGITQCNIAHALEKTYKPPSDIYWKFEDEKHFSCQFTADIIAMNADFIIT 481
472 QY STYQBIAGSKNTVQGYESHATAFTLPGYRVVHGIDVDPKNIYSPGADMSIYPPHTEKA 531
482 DB STYQBIAGSKNTVQGYESHATAFTLPGYRVVHGIDVDPKNIYSPGADMTIYPPYSDKE 541
532 QY KRLTSHSGSIENLIYDPQNDHEHGLHDDRSKPIFLSMARLDVRVNIITGLVEAFKAKAK 591
542 DB KRLTALHSGSIENLIYDPQNDHEHGLHDDRSKPIFLSMARLDVRVNIITGLVEAFKAKAK 601
592 QY RELVNLVVAGVNDVKNYSKDRREIABIEMHKLKTHNLFGQFRMISAGTRARNGELRY 651
602 DB RELVNLVVAGVNDVKNYSKDRREIABIEMHKLKTHNLFGQFRMISAGTRARNGELRY 661
652 QY YIADTEGAFVQPALYAEAGLTVEAMTCGLPTFATLHGCPAEIIEHGVSGPHIDPHYHPEQ 711
662 DB YIADTKGAFVQPALYAEAGLTVEAMTCGLPTFATLHGCPAEIIEHGVSGPHIDPHYHPEQ 721
712 QY AVNLMAFFDRCKQCPDHVNVISAGLQRIYKYTWKIYSERLMTLAGYGVGWKVVSKLE 771
722 DB ASELAVDFFORCKEDDNHWNKVSDDGLQRIYKYTWKIYSERLMTLAGYGVGWKVVSKLE 781
772 QY RLETRRYLEMFIYLLKPRELAKTVPLA 797
782 DB RRETRRYLEMFIYLLKPRELANSVPIA 807

RESULT 3
T01420
sucrose synthase (EC 2.4.1.13) T2H3.8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999
C:Accession: T01420
R:Kalicki, J.; Gibson, A.
submitted to the EMBL Data Library, August 1998
A:Description: The sequence of A. thaliana T2H3.
A:Reference number: Z14324
A:Accession: T01420
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-808 <KAL>
A:Cross-references: EMBL:AF075597; NID:G3298610; PIDN:AAC28175.1; PID:G3377802
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 33/2; 77/3; 192/3; 304/3; 327/2; 421/3; 477/2; 552/2; 659/3; 741/2
A:Note: T2H3.8
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F;281-744/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 79.8%; Score 3366; DB 2; Length 808;
Best Local Similarity 78.9%; Pred. No. 4e-217;
Matches 620; Conservative 88; Mismatches 64; Indels 14; Gaps 2;

QY 7 DRYEDTLAHRNELVALLSKYVNGKGILOPHHILDALDEVQSG--GRALAEQPPDLVL 64
DB 14 DRYQDTLSAARNELVALLSKYVNGKGILOPHHILDELSVIGODETKKSLSDGPFPEIL 73

QY 65 RSQAEATVLPFPFVAIAVRPPGWYVYRVNVHLSVEQLTVSEYLRFPKELVDQSHNDPY 124
DB 74 KSMALVLPFPFVAIAVRPPGWYVYRVNVHLSVEQLTVSEYLRFPKELVDGPNSDPF 133

QY 125 VLDELDFEPNVSVPRNRSSIGNGVQFLNRHLSIMFRNRDCLLEPLDLFGRHRRHGHV 184

Db 134 CLELDPEFNANVPRPSSSSGNGVQFLNRHLSSVFNKCKDLEPLDLFLRVHXYKQHP 193
QY 185 MMLNDRIQSLGRQSVLTQKAEHLKSLPADTPYSQFAYKFOEWGLEKMGWGTAGHLEMI 244
Db 194 LMLNDRIQSLGRQSVLTQKAEHLKSLPADTPYSQFAYKFOEWGLEKMGWGTAGHLEMI 253
QY 245 HLLDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLDPTGGQIVVILDOVR 304
Db 254 HLLSDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLDPTGGQIVVILDOVR 313
QY 305 ALENEMVRLKKGGLDVSFKLIVITRLIPDAKTSQNRLEIRISCTOHTYILRVPEREN 364
Db 314 ALETEMILRLKKGGLDVSFKLIVITRLIPDAKTSQNRLEIRISCTOHTYILRVPEREN 361
QY 365 GILKKTWSRFQVWPYLETFABDAAGEAAEQGTDFIIGNYSDGNLVASLLSYKMGITQ 424
Db 362 GILKKTWSRFQVWPYLETFABDAAGEAAEQGTDFIIGNYSDGNLVASLLSYKMGITQ 421
QY 425 CNIAHALEKTYKYPDSIDFWKNDKXHFSCOPTADIAMNNADFIITSTYQEIAGSKNTV 484
Db 422 CTTAHALEKTYKYPDSIDFWKNDKXHFSCOPTADIAMNNADFIITSTYQEIAGSKNTV 481
QY 485 GOYESHAFITPLGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKRLTSLHGSIEHL 544
Db 482 GOYESHAFITPLGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKRLTSLHGSIEHL 541
QY 545 IYDPEQNDHEIGHLDSDRSKPIFLSMARLDVRKNTITGLVEAPAKCAKLELVNVLVAGYN 604
Db 542 IYDPEQNDHEIGHLDSDRSKPIFLSMARLDVRKNTITGLVEAPAKCAKLELVNVLVAGYN 601
QY 605 DVNKSXDREIEAEIKKHEHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 664
Db 602 DVNKSXDREIEAEIKKHEHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 661
QY 665 LYBAGLTVVWVAMTCGLPTFATLGGPAEIIHGHVSGFHIDPHYPEQAVNLMADFFDRCK 724
Db 662 LYBAGLTVVWVAMTCGLPTFATLGGPAEIIHGHVSGFHIDPHYPEQAVNLMADFFDRCK 721
QY 725 QDPDHWNIISAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKVSKLERLERRYLEMYI 784
Db 722 QDPDHWNIISAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKVSKLERLERRYLEMYI 781
QY 785 LKREL 790
Db 782 LKREL 787

RESULT 4

S71493
sucrose synthase (EC 2.4.1.13) - beet
C:Species: Beta vulgaris (beet)
C:Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
C:Accession: S71493; S71494
R:Hesse, H.; Willmitzer, L.
Plant Mol. Biol. 30, 863-872, 1996
A:Title: Expression analysis of a sucrose synthase gene from sugar beet (Beta vulgaris L.)
A:Reference number: S71493; MUID:96270366; PMID:8633746
A:Accession: S71493
A:Molecule type: mRNA
A:Residues: 1-822 <HES>
A:Cross-references: EMBL:X81974
R:Hesse, H.; Willmitzer, L.
submitted to the EMBL Data Library, September 1994
A:Description: Molecular cloning of a mitochondrial isoform of Cysteine Synthase from Ar
A:Reference number: S71494
A:Accession: S71494
A:Molecule type: mRNA
A:Residues: 'AG', 59-822 <HEW>
A:Cross-references: EMBL:X81974; NID:g1488569; PIDN:CAA57493.2; PID:g1488570
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:280-755/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 78.3%; Score 3302; DB 2; Length 822;
Best Local Similarity 78.3%; Pred. No. 7.8e-213;
Matches 624; Conservative 80; Mismatches 89; Indels 4; Gaps 3;
QY 7 DRVEDTLHAHNEVLVALLSKYVNGKGLIQPHHLLDALDEVQ--SGGRALAAEGPFLDVL 64
Db 13 ERVEDTLVHNEVLVALLSKYVNGKGLIQPHHLLDGLSVIGEDKQKILSDGPFSEVL 72
QY 65 RSAQEAIVLPFFVAIAVAPRGVMEYVVRVNHLSVSOQLTVSEYLRPKBELVDGQNDY 124
Db 73 RSAQEAIVLPFFVAIAVAPRGVMEYVVRVNHLSVSOQLTVSEYLRPKBELVDGQNDY 132
QY 125 VLELDFEENVSVPNRPSSSSGNGVQFLNRHLSSVFNKCKDLEPLDLFLRVHXYKQHP 184
Db 133 VLELDFEENVSVPNRPSSSSGNGVQFLNRHLSSVFNKCKDLEPLDLFLRVHXYKQHP 192
QY 185 MMLNDRIQSLGRQSVLTQKAEHLKSLPADTPYSQFAYKFOEWGLEKMGWGTAGHLEMI 244
Db 193 MMLNDRIQSLGRQSVLTQKAEHLKSLPADTPYSQFAYKFOEWGLEKMGWGTAGHLEMI 252
QY 245 HLLDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLDPTGGQIVVILDOVR 304
Db 253 HLLSDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLDPTGGQIVVILDOVR 312
QY 305 ALENEMVRLKKGGLDVSFKLIVITRLIPDAKTSQNRLEIRISCTOHTYILRVPEREN 364
Db 313 ALENEMVRLKKGGLDVSFKLIVITRLIPDAKTSQNRLEIRISCTOHTYILRVPEREN 372
QY 365 GILKKTWSRFQVWPYLETFABDAAGEAAEQGTDFIIGNYSDGNLVASLLSYKMGITQ 424
Db 373 GILKKTWSRFQVWPYLETFABDAAGEAAEQGTDFIIGNYSDGNLVASLLSYKMGITQ 432
QY 425 CNIAHALEKTYKYPDSIDFWKNDKXHFSCOPTADIAMNNADFIITSTYQEIAGSKNTV 484
Db 433 CNIAHALEKTYKYPDSIDFWKNDKXHFSCOPTADIAMNNADFIITSTYQEIAGSKNTV 492
QY 485 GOYESHAFITPLGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKRLTSLHGSIEHL 543
Db 493 GOYESHAFITPLGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKRLTSLHGSIEHL 552
QY 544 IYDPEQNDHEIGHLDSDRSKPIFLSMARLDVRKNTITGLVEAPAKCAKLELVNVLVAGYN 603
Db 553 IYDPEQNDHEIGHLDSDRSKPIFLSMARLDVRKNTITGLVEAPAKCAKLELVNVLVAGYN 612
QY 604 DVNKSXDREIEAEIKKHEHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 663
Db 613 DVNKSXDREIEAEIKKHEHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 672
QY 664 ALYBAGLTVVWVAMTCGLPTFATLGGPAEIIHGHVSGFHIDPHYPEQAVNLMADFFDRCK 723
Db 673 ALYBAGLTVVWVAMTCGLPTFATLGGPAEIIHGHVSGFHIDPHYPEQAVNLMADFFDRCK 731
QY 724 QDPDHWNIISAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKVSKLERLERRYLEMYI 783
Db 732 QDPDHWNIISAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKVSKLERLERRYLEMYI 791
QY 784 ILKRELAKTVPLADQ 800
Db 792 ILKRELAKTVPLADQ 808

RESULT 5

YUMU

sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C:Accession: S19125
R:Chopra, S.; Del-Favero, J.; Dolferus, R.; Jacobs, M.
Plant Mol. Biol. 18, 131-134, 1992
A:Title: Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.
A:Reference number: S19125; MUID:92119221; PMID:1531031
A:Accession: S19125

A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-804 <CHO>
A:Cross-references: EMBL:X60987; NID:g16525; PIDN:CZA43303.1; PID:g16526
C:Genetics:
A:Introns: 31/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2; 66
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:276-750/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 72.2%; Score 3045; DB 1; Length 804;
Best Local Similarity 73.3%; Pred. No. 1.2e-195;
Matches 571; Conservative 98; Mismatches 104; Indels 6; Gaps 4;

QY 24 LSKYVNGKGILOPHHIDALDEVOGSGGRALAEPPFLD 81
DB 29 LVRYVAHGKGILOSHQLIDFLKTVKVDGTLEDLNKSPFMKVL--QEAIVLPFPFVALAI 85
QY 82 RRRPGVWEYVRNVVHLSVEQLTVSEYLFKFEELVDGQNDPVVLELDFEPENVSVPREN 141
DB 86 RRRPGVWEYVRNVVHLSVEQLTVSEYLFKFEELVDGQNDPVVLELDFEPENVSVPREN 145
QY 142 RSGSINGVQFNLRLHSLSSIMFRNDCLEPLDFIRGHRKHGMVMDRIQSLGRQLSVL 201
DB 146 RSGSINGVQFNLRLHSLSSIMFRNDCLEPLDFIRGHRKHGMVMDRIQSLGRQLSVL 205
QY 202 TXABEHLKSLPADTPVSOFAYPQENGLEKMGWDTAGHVLVEMHLLDIIQADPSTLEK 261
DB 206 ARAAEFLSKPLATPYSEFEFELQCGFERGWDTAQKVSVMVHLLDIIQADPSTLEK 265
QY 262 FUGRIPMIENNVVSPHGVGQANVLGLDGTGGVIVVLDQVRALENEMVLRKKGGLDV 321
DB 266 FUGRIPMIENNVVSPHGVGQANVLGLDGTGGVIVVLDQVRALENEMVLRKKGGLDV 325
QY 322 SPKILIVITLIPDAKTSQNRLEISGTHYTLVRPFRNENGILKQWISRFVWPYLE 381
DB 326 IPKILIVITLIPDAKTSQNRLEISGTHYTLVRPFRNENGILKQWISRFVWPYLE 385
QY 382 TPAADAAGHIAELQTPDFTIGNYSDGNLVASLLSKYMGITQCN:AHALEKTYPDSI 441
DB 386 TPAADAAGHIAELQTPDFTIGNYSDGNLVASLLSKYMGITQCN:AHALEKTYPDSI 445
QY 442 FKNQPKYHFSQFQADIIAMNADFIITSTYQELAGSNVTVQYESHFTPLGLYRV 501
DB 446 YRNHEDKTHFSQFQADIIAMNADFIITSTYQELAGSNVTVQYESHFTPLGLYRV 505
QY 502 VHGDVDFKFNIVSPGADMSIYFPHTEKAKRLTSLHSGSIENLIYDPQNDHGHLD 561
DB 506 VHGDVDFKFNIVSPGADMSIYFPHTEKAKRLTSLHSGSIENLIYDPQNDHGHLD 565
QY 562 SKPILSMARLDVKNITGLVEAFKAKRELNVNVVAGYDVKNSKDRERIELEKM 621
DB 566 SKPILSMARLDVKNITGLVEAFKAKRELNVNVVAGYDVKNSKDRERIELEKM 625
QY 622 HELIKTHFGPQWISAOQNRNARNGELYRIADTHGAFQVAPALYFAFGLTVVEAMTCGL 681
DB 626 HSLIEQDLHGFERNAAQNRVNRNGELYRIADTKGVFPQAFYFAFGLTVVESMTCA 685
QY 682 PTFATLGGPAAIEIHGVSGFHDIPVHPEQAQVNLMAOFFJCRKODPDHWNISAGLORI 741
DB 686 PTFATLGGPAAIEIHGVSGFHDIPVHPEQAQVNLMAOFFJCRKODPDHWNISAGLORI 744
QY 742 YERYTWKYSERLMTAGVYGFKNYSKLELLETRVRYLEMYLILKPELAKTVPLADQ 800
DB 745 YERYTWKYSERLMTAGVYGFKNYSKLELLETRVRYLEMYLILKPELAKTVPLADQ 803

RESULT 6
YUZMS
sucrose synthase (EC 2.4.1.13) - maize
C:Species: Zea mays (maize)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C:Accession: S07184; S19085

R:Werr, M.; Prommer, W.B.; Maas, C.; Starlinger, P.
EMBO J. 4, 1373-1380, 1985
A>Title: Structure of the sucrose synthase gene on chromosome 9 of Zea mays L.
A:Reference number: S07184
A:Accession: S07184
A:Molecule type: DNA
A:Residues: 1-802 <WER>
A:Cross-references: EXBL:X02382; NID:g22487; PIDN:CAA26229.1; PID:g22488
A:Accession: S19085
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-802 <WER>
A:Cross-references: EMBL:X02400; NID:g22485; PIDN:CAA26247.1; PID:g22486
C:Genetics:
A:Gene: sh
A:Map position: 9
A:Introns: 32/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2; 66
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:276-750/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 71.0%; Score 2993.5; DB 1; Length 802;
Best Local Similarity 70.0%; Pred. No. 3.3e-192;
Matches 558; Conservative 105; Mismatches 131; Indels 3; Gaps 2;

QY 3 HASGDRVDTLHARRNELVALLSKYVNGKGILOPHHIDALDEVOGSGGRALAEPPFLD 62
DB 9 HSLRELGATFSSHFNELALFSRYVHQKGLQRLHLLAEFDALFSDKEKVA--PFED 66
QY 63 VLRSQAELVLPFWALAVRPPGVWYVRNVVHLSVEQLTVSEYLRKFEELVDGQND 122
DB 67 ILRAAQEALVLPFWALAVRPPGVWYVRNVVHLSVEQLTVSEYLRKFEELVDGQNS 126
QY 123 PVVLELDFEPENVSVPRENSSINGVQFNLRLHSLSSIMFRNDCLEPLDFIRGHRKHG 182
DB 127 NFVLELDFEPENVSVPRENSSINGVQFNLRLHSLSSIMFRNDCLEPLDFIRGHRKHG 186
QY 183 HVVMDLRISQRLQSLVLTAKAEHLKSLPADTPVSOFAYPQENGLEKMGWDTAGHVLV 242
DB 187 TVVMDLRISQRLQSLVLTAKAEHLKSLPADTPVSOFAYPQENGLEKMGWDTAGHVLV 246
QY 243 MIHLLDIIQADPSTLEKFLGIPMIENNVVSPHGVGQANVLGLDGTGGVIVVLDQ 302
DB 247 TLHLLDIIQADPSTLEKFLGIPMIENNVVSPHGVGQANVLGLDGTGGVIVVLDQ 306
QY 303 VRALENEMVLRKKGGLDVSPKILIVITLIPDAKTSQNRLEISGTHYTLVRPFRN 362
DB 307 VRALENEMVLRKKGGLDVSPKILIVITLIPDAKTSQNRLEISGTHYTLVRPFRN 366
QY 363 ENGLKRWISRFVWPYLETFAEDAAGEIAAEIQTGTPDFTIGNYSDGNLVASLLSKYOGI 422
DB 367 ENGLKRWISRFVWPYLETFAEDAAGEIAAEIQTGTPDFTIGNYSDGNLVASLLSKYOGI 426
QY 423 TQCNIAHALEKTYPDSIIFKNPDEKIHFSQFQADIIAMNADFIITSTYQELAGSN 482
DB 427 TQCNIAHALEKTYPDSIIFKNPDEKIHFSQFQADIIAMNADFIITSTYQELAGSN 486
QY 483 TVQYSHSHTAFTPLGLYRVVHGDIVDPKFNIVSPGADMSIYFPHTEKAKRLTSLHSGSI 542
DB 487 TVQYSHSHTAFTPLGLYRVVHGDIVDPKFNIVSPGADMSIYFPHTEKAKRLTSLHSGSI 546
QY 543 NLIVYDQNDHGHLDHRSKPLFNSMARLDVKNITGLVEAFKAKRELNVNLVAVAG 602
DB 547 ELIVYDQNDHGHLDHRSKPLFNSMARLDVKNITGLVEAFKAKRELNVNLVAVAG 606
QY 603 YNDVNSKDRERIELEKMHLKTHNLFCQFPHISAOQNRNARNGELYRIADTHGAFQV 662
DB 607 -DEGKESKDRERIELEKMHLKTHNLFCQFPHISAOQNRNARNGELYRIADTHGAFQV 665
QY 663 PALYEAFLTVVEAMTCGLPTEATLHGGPAEIIHGVSGFHDIPVHPEQAQVNLMAOFF 722
DB 666 PALYEAFLTVVEAMTCGLPTEATLHGGPAEIIHGVSGFHDIPVHPEQAQVNLMAOFF 725

Db 14 HSVREIGSLSAHNELVAVTRLVNKGMLQAHQIIAYNNALSEADREKLDGAFE 73
 Qy 62 DVLSAQBAIVLPPFAIAVPRPGVWEYVRNVNHELSSVEQLTVSEYLRFKELVDGQIN 121
 Db 74 DVLSAQEGIVISPVVALAIRPRPGVWEYVRNVNSELAVELLTVPEYLQFKQLVEEGTN 133
 Qy 122 DRYVLELDEPENUSVPRNRSSTGNGVQFLNRHLSSIMERNRDCLEPLDPLRHRHK 181
 Db 134 NNFVLELDEPPNABFPRESLSKSGNGVQFLNRHLSSKFLFDKSMYPLNPLRAHNYK 193
 Qy 182 GHWMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEMGLEKGGDGTAGHYL 241
 Db 194 GWTMLNDIRLSLSALQALRAEHLKSLGSDTPYSEFHRFQELGLEKGGDCAKRSQ 253
 Qy 242 EMHLLDIIQAPDSTLEKFLGRIPMIENVVVSHPGYFGQANVLGLDPTGGQIVYILD 301
 Db 254 ETIHLLDLEAPDSTLEKFLGTIPMVFNVMVIMSPHYFAQANVLGYDPTGGQVYILD 313
 Qy 302 QVRALENEMVLRKKQGLDVSPIKLVTRLIIPDAKGTSCNORLERISGTOHTVILRVPR 361
 Db 314 QVRAMENMLLRKQGLDVSPIKLVTRLIIPDAKGTSCNORLERISGTOHTVILRVPR 373
 Qy 362 NENGILKKWISRDVWPYLETFAEDAAGEIAEABELOCTPDFIIGNYSDGNLVALSLYXMG 421
 Db 374 TENGIVRKWISREVPWYLETPTDDVAHELAGELQAMPDLIIIGNYSDGNLVALCLAHKM 433
 Qy 422 ITQCNIAHALEKTKYPSDILFWKDFEKFHSCOPTADIIAMNADFIITSTVOELAGSK 481
 Db 434 VTHCTIAHALEKTKSPNSOLYWKKFDHYFSCQPTTDLIAMNADFIITSTVOELAGN 493
 Qy 482 NTVGQYESHTAFTPLGLYRVVHGIDVDPKENTVSPGADMSIYPHTEKAKRLTSLHGI 541
 Db 494 DTVGQYESHMAFTMPGLYRVVHGIDVDPKENTVSPGADMSIYPHTEKAKRLTSLHPEI 553
 Qy 542 ENLIYDPEQNDHEIGHLDSDSKILFSMARLDVKNITGLVEAFKAKRLRELNLVVVA 601
 Db 554 EELLYSEVONNEHKFMLKDRNKPIIFSMARLDVKNITGLVEAFKAKRLRELNLVVVC 613
 Qy 602 GYNDVNSKDRBEIAEIKOMHELKTNLFGQFWRWISQATNRANGELYRYIADTHGAFV 661
 Db 614 G-DHGNSPKDKEQAEKQKFDLEQNLNGHRTWISQATNRANGELYRYIADTHGAFV 672
 Qy 662 OPALYEAFTLVVEAMTCGLPTFATLGGPAEIIIEHGVSGPHIDPHPEQANVLMAFFD 721
 Db 673 OPALYEAFTLVVEAMTCGLPTFATLGGPAEIIIEHGVSGPHIDPHPEQANVLMAFFD 732
 Qy 722 RCKQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRYLEM 781
 Db 733 KCQDPDHWTKISQGLQRIEYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRYLEM 792
 Qy 782 FYILKRELAKTVPLAID 799
 Db 793 LYALKYRTMASTVPLAVE 810

RESULT 9

YUPOS

sucrose synthase (EC 2.4.1.13) - potato

C:Species: Solanum tuberosum (potato)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999

C:Accession: A29615

R:Salanoubat, M.; Belliard, G.

Gene 60, 47-56, 1387

A:Title: Molecular cloning and sequencing of sucrose synthase cDNA from potato (Solanum

A:Reference number: A29615; PMID:88152501; PMID:2964386

A:Accession: A29615

A:Molecule type: mRNA

A:Residues: 1-805 <SAL>

A:Cross-references: GB:M18745; NID:g169571; PIDN:AAA33841.1; PID:g169572

A:Experimental source: var. Sirrema 2n=4x

C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

C:Keywords: glycosyltransferase; hexosyltransferase

F:279-753/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 69.8%; Score 2944.5; DB 1; Length 805;

Best Local Similarity 68.9%; Pred. No. 6.4e-189;

Matches 549; Conservative 115; Mismatches 132; Indels 1; Gaps 1;

Qy 3 HASGSRVEDTLHAHRELVALSKYVKNKGILQPHHILDALDEVOGSGRALARAGPFLD 62
 Db 10 HSIRERVDATLAHRMEILLFLSIESHGKILKPHLEAEFAIRQDDCKNLNEHAFEE 69
 Qy 63 VLRSAGEAIVLPPFAIAVPRPGVWEYVRNVNHELSSVEQLTVSEYLRFKELVDGQIN 122
 Db 70 LKSTOEALVLPFWALAIRPGVWEYVRNVNHELSSVEQLTVSEYLRFKELVDGQIN 129
 Qy 123 EYVLELDEPPNABFPRESLSKSGNGVQFLNRHLSSIMERNRDCLEPLDPLRHRHK 182
 Db 130 NNFVLELDEPPNABFPRESLSKSGNGVQFLNRHLSSKFLFDKSMYPLNPLRAHNYK 189
 Qy 183 GHWMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEMGLEKGGDGTAGHYL 242
 Db 190 GWTMLNDIRLSLSALQALRAEHLKSLGSDTPYSEFHRFQELGLEKGGDCAKRSQ 249
 Qy 243 EMHLLDIIQAPDSTLEKFLGRIPMIENVVVSHPGYFGQANVLGLDPTGGQIVYILD 302
 Db 250 ETIHLLDLEAPDSTLEKFLGTIPMVFNVMVIMSPHYFAQANVLGYDPTGGQVYILD 309
 Qy 303 QVRALENEMVLRKKQGLDVSPIKLVTRLIIPDAKGTSCNORLERISGTOHTVILRVPR 362
 Db 310 QVRAMENMLLRKQGLDVSPIKLVTRLIIPDAKGTSCNORLERISGTOHTVILRVPR 369
 Qy 363 NENGILKKWISRDVWPYLETFAEDAAGEIAEABELOCTPDFIIGNYSDGNLVALSLYXMG 422
 Db 370 TENGIVRKWISREVPWYLETPTDDVAHELAGELQAMPDLIIIGNYSDGNLVALCLAHKM 429
 Qy 423 ITQCNIAHALEKTKYPSDILFWKDFEKFHSCOPTADIIAMNADFIITSTVOELAGSK 482
 Db 430 VTHCTIAHALEKTKSPNSOLYWKKFDHYFSCQPTTDLIAMNADFIITSTVOELAGN 489
 Qy 483 NTVGQYESHTAFTPLGLYRVVHGIDVDPKENTVSPGADMSIYPHTEKAKRLTSLHGI 542
 Db 490 DTVGQYESHMAFTMPGLYRVVHGIDVDPKENTVSPGADMSIYPHTEKAKRLTSLHPEI 549
 Qy 543 ENLIYDPEQNDHEIGHLDSDSKILFSMARLDVKNITGLVEAFKAKRLRELNLVVVA 602
 Db 550 EELLYSEVONNEHKFMLKDRNKPIIFSMARLDVKNITGLVEAFKAKRLRELNLVVVC 609
 Qy 603 GYNDVNSKDRBEIAEIKOMHELKTNLFGQFWRWISQATNRANGELYRYIADTHGAFV 662
 Db 610 G-DHGNSPKDKEQAEKQKFDLEQNLNGHRTWISQATNRANGELYRYIADTHGAFV 668
 Qy 663 OPALYEAFTLVVEAMTCGLPTFATLGGPAEIIIEHGVSGPHIDPHPEQANVLMAFFD 722
 Db 669 OPALYEAFTLVVEAMTCGLPTFATLGGPAEIIIEHGVSGPHIDPHPEQANVLMAFFD 728
 Qy 723 RCKQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRYLEM 782
 Db 729 RCKQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRYLEM 788
 Qy 783 FYILKRELAKTVPLAID 799
 Db 789 LYALKYRTMASTVPLAVE 805

RESULT 10

S31479

sucrose synthase (EC 2.4.1.13) - fava bean

C:Species: Vicia faba (fava bean)

C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999

C:Accession: S31479

R:Heim, U.; Weber, H.; Wobus, U.

submitted to the EMBL Data Library, December 1992

A:Description: Sucrose synthase expression patterns in developing seeds of Vicia faba ir

A:Reference number: S31479

Db 789 YLEMYALKYRKAAATVPLAVE 810
 RESULT 12
 S37560
 sucrose synthase (EC 2.4.1.13) - carrot
 C:Species: Daucus carota (carrot)
 C:Date: 09-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C:Accession: S37560
 R:Sturm, A.
 submitted to the EMBL Data Library, October 1993
 A:Description: Nucleotide sequence of a cDNA clone coding for sucrose synthase from carrot
 A:Reference number: S37560
 A:Accession: S37560
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-808 <STU>
 A:Cross-references: EMBL:X75332; NID:g406316; PIDN:CAA53081.1; PID:g406317
 C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 C:Keywords: glycosyltransferase; hexosyltransferase
 F:281-755/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
 Query Match 69.0%; Score 2910.5; DB 2; Length 808;
 Best Local Similarity 67.8%; Pred. No. 1.2e-186;
 Matches 542; Conservative 114; Mismatches 141; Indels 3; Gaps 2;
 QY 3 HASGRVDTLHARNELVALLSKYVNGKGLQPHHILDALDEVQSGGRAL--AEGPF 60
 Db 10 HSLREDMOSTLANHREILMELRIEISHGKGLKPHQLLAEXEAIKEDKXLDGCGAF 69
 QY 61 LDVLSAQEAIVLPPTAVATVRPPGVWEYRVNVVHLSVEQLTVSEYLFKKEELVDGQH 120
 Db 70 AEVKSQTQEAIVSPWVALAIRLPGWYRVNVVHLSVEQLTVSEYLFKKEELVIGSS 129
 QY 121 NPYVLELDFEPNVPVPRNRSISNGVQFVNLRLSSIMFNRDCEPLDPLFLGRHRH 180
 Db 130 DANFVLELDFAPTAFFPTLTKSINGVEFLNRHLSAKMFGKDSMHLEFLFLRNY 189
 QY 181 KGVMMNDRIQSLGRQSVLTKAEBHLSKLPADTPYSQPAYKFOEWGLKKGMDTAGHV 240
 Db 190 NGKTLMLNRRVNVNGQLQMLRAGDYLSTLPDTPYSEFEHFKFOETGFERGMDTAERV 249
 QY 241 LEMHLLDIIQAPDSTLEKELGRIPMIVNVVSPHGVFGANVLGLPDTGQIVYL 300
 Db 250 TENFHLDDLEAPDASTLTFTFGKIPMIVNVVSPHGVFGANVLGLPDTGQIVYL 309
 QY 301 DQVRALENEMVLRLKXQGLDVSFKILITVRLIPDAKGTSCNORLERISGTQHYILRVPF 360
 Db 310 DQVPALEREMIKELKEQGLDIPKILITVRLIPDAVGTTCNORLEKVFGAZHAHLRVPF 369
 QY 361 RNENGILKWIISFDPVWPYLETFAEDMAEIAELQCTPDPIIGNYSDGNIVASLLSYKM 420
 Db 370 RTEKGILRWISRFVWPYLETETEDVAKELALELQAKPDIIIGNYSEGNIVASLLAHL 429
 QY 421 GITQCNIAHALEKTKYDSDIPKNDPEKHFSCQFTADIIAMNADPITTSYQEIAGS 480
 Db 430 GVTCCTIAHALEKTKYDSDIDYKFKPKKHFSCQFTADIIAMNADPITTSYQEIAGS 489
 QY 481 KNTVGQVESHTAFTLPGLXRVVHGDVDFDPKFNIVSPGADMSIYFPHTKAKRLTSLHGS 540
 Db 490 KNTVGQVESHTAFTMPGLXRVVHGDVDFDPKFNIVSPGADMSIYFVYKEKRLTTLHPE 549
 QY 541 IENLIYDPEQNDHEIGHLLDRSKPLFSMARLDRVQNTGLVEFAFACAKRELNVLVVY 600
 Db 550 IEELLYSSVNEEHLCKIKDKNKPILFTMARLDNVKNTLGFVEVYAKSPKRELNVLVVY 609
 QY 601 AGYNDVNSKDRRELAIEIKMHELIKTHNLFGQFRTISAQTNARNGELYIADTHGAF 660
 Db 610 GG-DRRKESKDLBEQAQKKMYELIDYKNGQFRWISSQNNVRNRELVRVYADTGGAF 668
 QY 661 VQPALYEAFLGVVVEAMTCGLPTFATLHGGAFAEIIIEHGVSGFHLDPYHQBQAVNLMADFF 720

Db 669 VQPAFYFAFGLTVVEAMTCGLPTFATLHGGAFAEIIIVHKGSGPHIDPHGQVAAELLVNF 728
 QY 721 DRCKODPDHWNVISGAGLQRIYKTYTWKYSERLMTLAGVYGPWKVSKLERLETRYLE 780
 Db 729 EKCKTDPQMDAISAGLAKRIEKTYTWKYSERLMTLAGVYGPWKVSKLERLETRYLE 788
 QY 781 MFYILKFRLEIAKTVPLAIDQ 800
 Db 789 MFYALKYRKLAESVPLAKDE 808
 RESULT 13
 T49233
 sucrose synthase-like protein - Arabidopsis thaliana
 X:Alternate names: protein F7K15.40
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T49233
 R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeidler, K.; Mewes, H.W.; Rudd, S.; Len
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25019
 A:Accession: T49233
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-808 <OBE>
 A:Cross-references: EMBL:AL353871; GSPDB:GN00061; ATSP:F7K15.40
 A:Experimental source: cultivar Columbia; BAC clone F7K15
 C:Genetics:
 A:Gene: ATSP:F7K15.40
 A:Map position: 3
 A:Introns: 35/2; 128/2; 192/3; 304/3; 336/3; 394/3; 433/3; 489/2; 564/2; 752/2; 798/3
 C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 Query Match 68.9%; Score 2904.5; DB 2; Length 808;
 Best Local Similarity 68.3%; Pred. No. 3e-186;
 Matches 545; Conservative 112; Mismatches 140; Indels 1; Gaps 1;
 QY 3 HASGRVDTLHARNELVALLSKYVNGKGLQPHHILDALDEVQSGGRALAEAGPFLD 62
 Db 12 HSQERLDATLVAQKNEVFALLSRVEAKGKGLQHHQIIAEFEAMPLETQKXKLGGAFFE 71
 QY 63 VLSAQEAIVLPPTAVATVRPPGVWEYRVNVVHLSVEQLTVSEYLFKKEELVDGQND 122
 Db 72 FLRSAQEAIVLPPTAVATVRPPGVWEYRVNVVHLSVEQLTVSEYLFKKEELVDGKNG 131
 QY 123 PYVLELDFEPNVPVPRNRSISNGVQFVNLRLSSIMFNRDCEPLDPLFLGRHRHG 182
 Db 132 NPTLELDFEPNAAFPRTLUNKYIGDGVFENRHLSSAKLFDKESLHPLXFLHSHSEG 191
 QY 183 HVMMNDRIQSLGRQSVLTKAEBHLSKLPADTPYSQPAYKFOEWGLKKGMDTAGHVLE 242
 Db 192 KTLMLNRIQNLTQHNLRKAEYLMELKPELTYSFEHFKFOETGFERGMDTAERVLN 251
 QY 243 MIHLLDIIQAPDSTLEKELGRIPMIVNVVSPHGVFGANVLGLPDTGQIVYLIDQ 302
 Db 252 MIRLLDLEAPDCTLENFLGRIPMIVNVVSPHGVFGANVLGLPDTGQIVYLIDQ 311
 QY 303 VRALENEMVLRLKXQGLDVSFKILITVRLIPDAKGTSCNORLERISGTQHYIILRVFPN 362
 Db 312 VRALETMLQRIKQOGLNITPRILITVRLIPDAVGTTCNORLEKVFYQYCDILRVFRT 371
 QY 363 ENGLIKKWIISFDPVWPYLETFAEDMAEIAELQCTPDPIIGNYSDGNIVASLLSYKMI 422
 Db 372 EKGIVRWISRFVWPYLETETEDVAAEISKEIQKPDIIIGNYSDGNIVASLLAHLGV 431
 QY 423 TQCNIAHALEKTKYDSDIPKNDPEKHFSCQFTADIIAMNADPITTSYQEIAGSKN 482
 Db 432 TQCTIAHALEKTKYDSDIYKFKLDEKHFSCQFTADIIAMNADPITTSYQEIAGSKD 491
 QY 483 TVGQYSSHTAFTLPGLXRVVHGDVDFDPKFNIVSPGADMSIYFPHTKAKELTSLHGSIE 542
 Db 492 TVGQYSSHTAFTLPGLXRVVHGDVDFDPKFNIVSPGADMSIYFAYTEKRLTAFHLEIE 551

191	N	R	V	O	T	V	N	G	L	O	I	I	R	I	A	G	E	Y	S	K	L	P	S	D	T	P	Y	S	D	F	H	K	F	O	E	I	G	F	E	R	G	W	G	T	A	H	V	S	E	M	F	H	L	255				
248	L	D	I	I	C	A	P	D	P	S	T	L	E	F	L	G	R	I	P	M	I	N	V	V	V	V	P	H	G	I	F	C	Q	A	N	V	L	G	L	P	D	T	G	G	O	V	I	L	D	O	V	R	A	L	E	307		
251	L	D	L	E	A	P	D	A	C	T	L	E	F	L	G	K	I	P	M	I	N	V	V	V	P	H	G	I	F	C	Q	A	N	V	L	G	L	P	D	T	G	G	O	V	I	L	D	O	V	P	A	M	E	310				
308	N	E	M	V	L	R	K	K	O	G	L	D	S	P	K	L	I	V	T	R	L	P	D	A	K	G	H	S	C	H	O	R	L	E	R	I	S	T	O	H	T	Y	L	R	P	P	R	E	N	G	I	L	367					
311	R	E	M	T	K	R	I	E	Q	E	G	L	D	I	P	R	-	L	I	V	T	R	L	P	D	A	V	G	T	C	N	L	R	E	K	V	F	G	A	E	H	S	H	I	L	R	P	P	T	E	K	G	I	L	370			
368	K	K	I	S	R	D	P	W	P	Y	L	E	T	F	A	E	D	A	A	E	T	A	E	L	O	G	T	P	D	F	I	I	G	N	S	D	G	N	L	V	A	S	L	L	S	K	W	M	G	I	T	Q	C	N	I	427		
371	K	K	I	S	R	E	V	W	P	M	E	T	F	E	D	V	A	K	E	L	K	A	P	D	L	I	I	G	N	S	E	G	N	L	V	A	S	L	L	K	V	A	S	L	L	K	V	T	Q	C	T	I	430					
428	A	H	A	L	E	K	T	P	S	D	I	F	W	K	N	F	D	E	K	Y	H	F	S	C	O	F	T	A	D	I	I	A	M	N	A	D	F	I	T	S	T	Y	O	E	I	A	G	S	K	N	T	V	G	Y	487			
431	A	H	A	L	E	K	T	P	S	D	I	F	W	E	K	F	D	K	K	Y	H	S	S	C	O	F	T	A	D	I	I	A	M	N	H	T	D	F	I	T	S	T	F	O	E	I	A	G	S	K	D	T	V	G	Y	490		
488	E	S	H	T	A	F	I	L	P	G	L	Y	R	V	H	G	I	D	V	D	P	K	N	I	S	P	G	A	D	M	S	I	Y	F	Z	H	E	K	A	R	L	S	L	H	G	S	I	E	N	L	A	Y	D	547				
491	E	S	H	T	A	F	M	P	G	L	Y	R	V	H	G	I	D	V	D	P	K	N	I	S	P	G	A	D	T	S	V	I	Y	F	T	E	K	K	R	L	T	A	L	H	E	I	D	L	L	F	S	550						
548	P	E	O	N	D	E	H	I	G	H	L	D	R	S	K	P	I	L	F	S	M	A	R	L	D	R	V	K	N	T	I	G	L	V	E	A	P	A	K	A	C	A	K	R	E	L	N	L	V	V	V	A	G	N	D	V	N	607
551	S	V	E	N	K	E	H	L	C	V	L	K	O	R	Y	K	P	I	L	F	T	M	A	R	L	D	N	V	K	N	L	T	G	I	V	E	W	A	K	P	K	A	R	E	L	N	L	V	V	V	G	-	D	R	E	K	609	
608	K	S	K	O	R	E	E	T	A	E	I	E	K	M	H	E	L	I	K	T	H	N	L	F	O	G	F	R	N	I	S	A	O	T	N	R	A	N	G	E	L	Y	R	I	A	O	T	H	G	A	F	O	P	A	L	E	667	
61																																																										

Search completed: May 24, 2004, 11:29:38
Job time : 19.424 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 19.4153 seconds
(without alignments)
2132.550 Million cell updates/sec

Title: US-10-080-114A-2

Perfect score: 4217

Sequence: 1 STHASGURVEDTLHAHREL.....YILKRELAKTVPLAIDQPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3158	74.9	766	2	US-08-553-436A-8
2	2879.5	68.3	805	4	US-09-598-401C-77
3	1833	43.5	806	4	US-08-684-005-2
4	467.5	11.1	720	4	US-09-394-272-14
5	466.5	11.1	1083	4	US-09-394-272-11
6	450	10.7	1056	4	US-09-394-272-1
7	447.5	10.6	963	4	US-09-394-272-12
8	447.5	10.6	963	4	US-09-394-272-13
9	444	10.5	1059	4	US-09-394-272-5
10	444	10.5	1068	2	US-08-429-054A-11
11	444	10.5	1068	2	US-08-718-777-7
12	444	10.5	1068	3	US-09-051-341-7
13	444	10.5	1068	4	US-09-394-272-8
14	441.5	10.5	1045	2	US-08-553-436A-6
15	441.5	10.5	1045	4	US-09-394-272-7
16	438	10.4	1054	1	US-08-356-354-4
17	438	10.4	1054	2	US-08-778-656-4
18	436.5	10.4	1053	4	US-09-394-272-6
19	425	10.1	1054	4	US-09-394-272-3
20	420	10.0	1059	4	US-09-697-367-16
21	414	9.8	1057	4	US-09-697-367-23
22	414	9.8	1057	4	US-09-394-272-2
23	411	9.7	1057	3	US-08-853-948B-2
24	408.5	9.7	1081	4	US-09-394-272-4
25	401.5	9.5	1084	4	US-09-394-272-9
26	396	9.4	846	1	US-08-356-354-2
27	396	9.4	846	2	US-08-778-656-2

28	351	8.3	1049	4	US-09-394-272-10	Sequence 10, Appl
29	342	8.1	125	4	US-09-598-401C-76	Sequence 76, Appl
30	307	7.3	908	1	US-08-356-354-6	Sequence 6, Appl
31	307	7.3	908	2	US-08-778-656-6	Sequence 6, Appl
32	280	6.6	668	4	US-09-697-367-2	Sequence 2, Appl
33	262.5	6.2	368	4	US-09-697-367-24	Sequence 24, Appl
34	256	6.1	343	3	US-08-853-948B-10	Sequence 10, Appl
35	251	6.0	341	3	US-08-853-948B-4	Sequence 4, Appl
36	233.5	5.5	365	4	US-09-697-367-8	Sequence 8, Appl
37	222	5.3	343	3	US-08-853-948B-3	Sequence 3, Appl
38	221	5.2	348	3	US-08-853-948B-5	Sequence 5, Appl
39	172	4.1	210	4	US-09-697-367-10	Sequence 10, Appl
40	161	3.8	507	4	US-09-134-001C-3978	Sequence 3978, Ap
41	160.5	3.8	358	4	US-09-697-367-20	Sequence 20, Appl
42	155	3.7	59	3	US-09-125-984-2	Sequence 2, Appl
43	152.5	3.6	502	4	US-09-134-001C-4511	Sequence 4511, Ap
44	149.5	3.5	369	4	US-09-543-681A-7514	Sequence 7514, Ap
45	148	3.5	393	4	US-09-252-991A-19043	Sequence 19043, A

ALIGNMENTS

RESULT 1

US-08-553-436A-8
Sequence 8, Application US/08553436A
Patent No. 5866790

GENERAL INFORMATION:

APPLICANT: HESSE, Holger
APPLICANT: MULLER-KOBER, Bernd
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
TITLE OF INVENTION: CONCENTRATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oetrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8403

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/553.436A

APPLICATION NUMBER: US/08/553.436A

FILING DATE: 17-NOV-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP94/01671

FILING DATE: 20-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 4317596.1

FILING DATE: 24-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Meilman, Edward

REGISTRATION NUMBER: 24,735

REFERENCE/DOCKET NUMBER: P/951-117

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 382-0700

TELEFAX: (212) 382-0888

TELEX: 236925

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 766 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-553-436A-8

Query Match

74.9%; Score 3158; DB 2; Length 766;


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Db      255  IILALSRPDPKNIHLKIAAGQSPOLQAQANLVIVAG-----NRDDITDLDQGPRE 306
Qy      620  KMEHIXT---HNLFQGPFWTSAOTNRARN-GEHYRYIADTHGAFVQPALYAEAFGLTVVE 675
Db      307  VLTDLTLTIDRYDLYGKWAY--PKQQAEDVVALFRLTALSQGVFINDALEPFGGLTIE 364
Qy      676  AWTGCLPTFATLHGGPARIIEHGVSGFHDIPYHPOAVNLMAADFDRCQKQDPDHWNLSE 735
Db      365  AARCGVPVATVDEGDFVDIINKCONGYLINPLDEVD---IADKLVKINDKQKQOFUSE 420
Qy      736  AGLCRIYKTYKWKYSERLMTLAGYGVFWKVKSKLERLETRYLSEMFY 783
Db      421  SGLEGVKHYSWPSEVSY--LEAINALTQTSVLKRSDLKERRILY 466

RESULT 5
US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-394-272-11

Query Match      11.1%; Score 466.5; DB 4; Length 1083;
Best Local Similarity 24.3%; Pred. No. 5.2e-34;
Matches 184; Conservative 130; Mismatches 285; Indels 159; Gaps 32;

Qy      111  FKSELVDG-QHNDPVYLEDFFPNVSVPRNRSSTI-----GNGVQLP 153
Db      67  FVEEVNVSFSDLYKTKWIKVIATNTRERSNRLENICAKIWLARKKQIVWDDGVRLS 126
Qy      154  NRELSSIMFRNDCLEPILDEL-RGRHKGHWMLNDRQSLGRLOSVLTKAEHLSKLP 212
Db      127  KRRIEREQGN-DAEEDLLSELSEGEKDK-----NDGEKSEVVTTLEPRDRHPRIR 179
Qy      213  ADTPYSQPAYKFOEWLEKMGWGTAGHLEMIHLDDIIQAAPPSTLEKFLGRIPFNW 272
Db      180  SE-----NQIWESED-----DKSSR-----NLYIVLRQVEIGFSDLF-----VFENM 216
Qy      273  VV-----VSPHGYF-GQANVLGL-PDTGGQIVYLDQVRALEHMLVRLKK 316
Db      217  LVGLTWCLYLVPCFTNCSMEGLVRGENMELGRDSTGGQVKYVWELARALAN-----T 269
Qy      317  QGLDVSPKLIIVTRLPDAK-GTSCNQRLEIS---GTQH---TYILVRPERNENGILKK 363
Db      270  EGVH---RDVLTQRISSPEVDYSYGEPEVMISLCPPEGSNDSGSIYIIRIPC-----GSRDK 322
Qy      370  WISRPDVPVPLETFAEDAAGEIAA-----STQG-----TPDFIIGNYSDGNLVALLSY 418
Db      323  YIPKESLWPHIPFVDGALNHVSIARSLGEQVNGGKPIWPYVIGHYADAGEVAHAHLG 382
Qy      419  KMGITCNIAHALEKTYK-----PDSDFWKNFDEKHFSCQFTADIIAMNADFIITSTY 474
Db      383  ALNVPWLVTHSLGRNKFEOQLQGRITREDIDRTYKIMRIEAEQSLDAEAMVVTSTR 442
Qy      475  QETAGSNVWQYESTAFPLGLYRVHGDIV-----FDPKFNIV 515
Db      443  QEID-----AQW-----GLY---DGFDKLERKLVRRRRGVSCIGRYMPRWVVI 484
Qy      516  SPGADMSIYPPH--TEKAKRLTSLHGSIENTLIYDPEQN--DEHIGHLDDRSPILFSMAR 571
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Db      485  PPGMDFSYVLVTDQSDQPDGDLKSLIGPDRNQLKPPVPIWSEIMRFFSPHPFTILALSR 544
Qy      572  LDRVKNITGLVEAFAPAKAKLRELVNLVVVAGVNDVUNKSKOREIEAIEKMHKHLKTHNLP 631
Db      545  PDHKNVTTLVKAFGEQCQPLRELANLVILGNRDDIEEMPNSSSVVLMMVNLKLDQDYDY 604
Qy      632  GQFRWISAQTNRANGELYRYIADTHGAFVQPALYAEAFGLTVVEAMTCGLPTFATLHGGP 691
Db      605  GQVAY-PKHKQSEVVDIYRLAAKTGVFINPALVEPFGLLILIEAAAYGLPIVAITN3SF 663
Qy      692  AEIIIEHGVSGEHIIDPHYPEQAVNLMAADFDRCQKQDPDHWNLISGAGLQRIYKYTKWIIYS 751
Db      664  VDIVKALNGLLVDP-HDQQAII---SDALLX-VANKHLWAECKKNGLKNIH-RFSWPEHC 718
Qy      752  ERLMTLAGYGVFWKVKSKLERLETRYLSEMFYILAFRE 789
Db      719  R-----NYLSHVEHCNRHPTSSLDIMKYPE 744

RESULT 6
US-09-394-272-1
; Sequence 1, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-394-272-1

Query Match      10.7%; Score 450; DB 4; Length 1056;
Best Local Similarity 26.4%; Pred. No. 1.7e-32;
Matches 145; Conservative 97; Mismatches 218; Indels 90; Gaps 18;

Qy      272  VVWSPHGYF-GQANVLGL-PDTGGQIVYLDQVRALENE-----MYLRLKKQGLDV 321
Db      176  VVLIISLHGLIRGENMELGRDSTGGQVKYVWELARALGSMGPYRVYDILLTRQVSAFGVW 235
Qy      322  S---PKILIVTRLPDAKGTSCNQRLEISGTQHTYILRVPPFNENGILKKNISRFEDVWP 378
Db      236  SYGEP-----TEMLSRNSENSTELGESSG---AVIIRIPF-----GPKDKYVAKELLWP 283
Qy      379  YLETRADDAAG-----EIAAELQTPDPIIGNYSDGNLVALLSYKMGITQCNI 427
Db      284  TYPEFDGALSHITKQMSKVLGEQIGGGLPWVPASVHGRYADAGSARLSGALNVPWVFT 343
Qy      428  AHAELETK---YPSDITFWKNFDEKHFSCQFTADIIAMNADFIITSTYQYIAGSKNT 483
Db      344  GHSIGRDKLDQLLKQGRLSREVDATYKIMRIEAEELCLDASEIYITSTROIEBQ--- 400
Qy      484  VQYESHTAFTPLGLYRVVHGDIV-----FDPKFNIVSPGADMSIY 524
Db      401  -----WQLYHGFDLVLERKLARMRRGVSGHGRFMPRMKAPPGMBFNHI 445
Qy      525  FPHTEKAKRLTSLHGSIE-NLIYDPEQNDEHIGHLDDRSPILFSMARLDRVKNITGLVE 583
Db      446  AP---EDADMDTIDGKHESNANPDPIVWSEIMRFFSNRGRKPMILALARPPEKKNLITLVK 503
Qy      584  APAKAKLRELVNLVVVAGVNDVUNKSKDRREEIAIEKMHKHLKTHLFGQFRWISAQTNR 643
Db      504  AFGECPRLRELANTLIIGNRDDIDEMSTSSSVLSILKLDKYDLYGQVAY-PKHKQ 562
Qy      644  ARNGELYRYIADTHGAFVQPALYAEAFGLTVVEAMTCGLPTFATLHGGPARIIEHGVSGFH 703
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QY 530 KAKRLTSLHSGSIENLIYDPEONDEHIG-----HLDKRSKPIFLFSMAR 571
 DB 449 -----EDIDGSDVKDIDVGLGASPKSMPPIAEVMRFLTNPKPMILALS 496
 QY 572 LDRVKNITGLVEAPAKCAKRELNLVNVVAGYNDVNSKDBEEIAEIEKHELIKTNLIF 631
 DB 497 FDPKNITTLVKAFGECPRLANLTLIMGNRDDIDMSAGNASVLTTLVKLIDKYDLY 556
 QY 632 GQFRWISAOQNRANGELYRIADTHGAFVOPALYEAAGLTVVEAMTGLPTFATLHGGP 691
 DB 557 GSVAF-PKHNNQADVPEIYLAAMKGVFINPALVEPPGLTLIAAAGLPIVATKNGGP 615
 QY 692 AEIIEHGVSGFHIDPYHPEQAVNLMADEFFDRCKQDPDHVNVNISGAGLQRIYEKTYWKIYS 751
 DB 616 VDIITNALNGLLVDPHQ-----NAIADALLKLVADKNLWQECRRNGLRNIH-LYSWPEHC 670
 QY 752 ERLMT-LAGVYGFWMKYVSKLERLSTRYLE 780
 DB 671 RYTLTRVAGC-----RLNRPWLK 689

RESULT 11

US-08-718-777-7
 ; Sequence 7, Application US/08718777
 ; Patent No. 5981852
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Asseche, C.
 ; APPLICANT: Lando, D.
 ; APPLICANT: Bruneau, J. M.
 ; APPLICANT: Voelker, T.
 ; APPLICANT: Gervais, M.
 ; TITLE OF INVENTION: MODIFICATION OF SUCROSE
 ; TITLE OF INVENTION: PHOSPHATE
 ; TITLE OF INVENTION: SYNTHASE IN PLANTS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Barbara Rae-Venter
 ; STREET: 260 Sheridan Avenue, Suite 440
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/718,777
 ; FILING DATE: NOT YET ASSIGNED
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/175,471
 ; FILING DATE: 27-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara Rae-Venter
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.072.02US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)328-4400
 ; TELEFAX: (415)328-4477
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1068 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-718-777-7

Query Match 10.5%; Score 444; DB 2; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 6.3e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 234 GDTAGHVLEMIHLLDIIQAPDPSTLEKFLGRIPMI-----FNVVVVSPHGYP- 281
 DB 141 GDTIGEL-----APVEITKKFQNFSDLTWSDDNKSKGLYVILSVHGLVR 188
 QY 282 QGANVLGH-PDTGGQIVYLDOVRALENEMVRLKKQGLDVP---KILIVTRLI--PD- 334
 DB 189 GENMELGRSDTGGQVKYVELARA-----MSMMPGVYRVDLFTROVSSPDV 235
 QY 335 -----AKGTSQNRLEISGTOHTYILRVPFERNENGLIKKWLSSRPDVPVLETF 383
 DB 236 DWSGEPTMELCAGSDGEGMGSGG---AYIVRIPC-----GPRDKYLKKEALWPLQGF 288
 QY 384 AEDAAGEI-----AAELQGT-----PDFIIGNYSDGNLVAISLLSYKMGITQCNIAHALE 432
 DB 289 VDGALAHILNMSKALGEQVGNRGPVLPVYVIGHYADAGDAALLSGALNPMVPLTCHSLG 348
 QY 433 KTK-----YDSDIIFWNFDEKHFSCQFTADIANNADFIITSTYQEIAGSKNTVGGYE 488
 DB 349 RNKLEQLLKQGRMSKEEIDSTYKIMRIEGEBELADASELVITSTROEID-----EQW- 401
 QY 489 SHTAFTLPLGLYRVVHGDV-----FDPKFNIVSPGADMSIYFPFHT 529
 DB 402 -----GLY---DGFVVKLEKVLARARGVSGHRYMPRMVWVIPPMDFSNVVH-- 448
 QY 530 KAKRLTSLHSGSIENLIYDPEONDEHIG-----HLDKRSKPIFLFSMAR 571
 DB 449 -----EDIDGSDVKDIDVGLGASPKSMPPIAEVMRFLTNPKPMILALS 496
 QY 572 LDRVKNITGLVEAPAKCAKRELNLVNVVAGYNDVNSKDBEEIAEIEKHELIKTNLIF 631
 DB 497 FDPKNITTLVKAFGECPRLANLTLIMGNRDDIDMSAGNASVLTTLVKLIDKYDLY 556
 QY 632 GQFRWISAOQNRANGELYRIADTHGAFVOPALYEAAGLTVVEAMTGLPTFATLHGGP 691
 DB 557 GSVAF-PKHNNQADVPEIYLAAMKGVFINPALVEPPGLTLIAAAGLPIVATKNGGP 615
 QY 692 AEIIEHGVSGFHIDPYHPEQAVNLMADEFFDRCKQDPDHVNVNISGAGLQRIYEKTYWKIYS 751
 DB 616 VDIITNALNGLLVDPHQ-----NAIADALLKLVADKNLWQECRRNGLRNIH-LYSWPEHC 670
 QY 752 ERLMT-LAGVYGFWMKYVSKLERLSTRYLE 780
 DB 671 RYTLTRVAGC-----RLNRPWLK 689

RESULT 12

US-09-051-341-7
 ; Sequence 7, Application US/09051341
 ; Patent No. 6124528
 ; GENERAL INFORMATION:
 ; APPLICANT: Shewmaker, C. K.
 ; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
 ; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rae-Venter Law Group, P. C.
 ; STREET: 260 Sheridan Avenue, Suite 440
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/051,341
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/17351
 ; FILING DATE: 25-OCT-1996

; APPLICATION NUMBER: US 08/549,016
 ; FILING DATE: 27-OCT-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/372,200
 ; FILING DATE: 12-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara Rae-Vetter, Ph.D.,
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.110.02US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)328-4400
 ; TELEFAX: (415)328-4477
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1068 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-051-341-7

Query Match 10.5%; Score 444; DB 3; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 6.3e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY	234	GDTAGHVLMIHLLDIIQAPDPSTLEKFLGRIPMI-----FNVVVSPHGYE- 281
Db	141	GTITIGEL-----APVETTKKFKQRFNSDLTWSSDDNKKKLYIVLIVSHGLVR 188
QY	282	GQANVLGL-PTGGQIVYILDQVRALENEMVLKKGGLDVP---KILIVTRLI--PD- 334
Db	189	GENMELGRSDTGGQVKYVVELARA-----MSMPGVYRVDLFTQVSSPDV 235
QY	335	-----AKGTSNORLERISGTQHTYILRVPRNENGILKKWISRFDPVPLTF 383
Db	236	DWSYGSPTMLCAGSDGCMGSGG---AYIVRIPC---GPRDKYLKKEALWPYLQEF 288
QY	384	ADDAAGEI-----AAELQGT-----PDFIIGNYSDGNLIVASLLSYKMGITOCNIAHALE 432
Db	289	VGCALAHILMSKALGEQVNGRPVLYVTHGYADAGVAAALLSGALNVPMVLTGHSLG 348
QY	433	KTK-----YPDSDFMKNFDEKHFSCQFTADIAMNADFIITSTQEIAGSKNTVGQYE 488
Db	349	RNKLEQLLKQGRMSKEEIDSTYKIMRRIEGEELALDASELIVITSTQEID-----EQW- 401
QY	489	SHTAFTPLGLYRVVHGIDV-----DGFVVKLEKVLARARRGVSGHGRYMRVVPVPGMDFSNVVVH-- 448
Db	402	-----GLY-----DGFVVKLEKVLARARRGVSGHGRYMRVVPVPGMDFSNVVVH-- 448
QY	530	KAKRLTSLHGSITENLYDPEQNDHEIG-----HLDERSKPIILFSMAR 571
Db	449	-----EDIDGDDGVKDDIVGLEGASPKSMPTIWAETVWRFLTNPHKPMILALS 496
QY	572	LDRVKNITGLVEAFKAKLRELNVLVVAGYNDVKNKSDREIEAEIKMHKILKTHNLF 631
Db	497	PDPKNITTLVKAFCGRPLRELANTLIMGNRDDIDDMASAGNASVLTTLVKLIDKYDLY 556
QY	632	GQPRWLSAQTNRARNCELRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTATLHGGP 691
Db	557	GSVAF-PKHNNQADVPEIYKLAAMKGVFINPALVEFFGLTIEAAAHGLPIVATKNGGP 615
QY	692	AEIIEHGVSGFHIDPYHPEQAVNLMAFFDRCQKDPDHWNVNISGAGLQRIYEKYITWKIYS 751
Db	616	VDITNALNGLLVDPHDQ-----NAIADALKLVADKNLMQECRRNGLRNIH-LYSWPEHC 670
QY	752	ERLMT-LAGVYGFWKVYKSLERLETREYLE 780
Db	671	RTYLTRVAGC-----RLRNPRLWK 689

RESULT 13
 US-09-394-272-8
 ; Sequence 8, Application US/09394272
 ; Patent No. 6472588

; GENERAL INFORMATION:
 ; APPLICANT: Haigler, Candace H.
 ; APPLICANT: Holaday, A. Scott
 ; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
 ; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
 ; FILE REFERENCE: 201304/1000
 ; CURRENT APPLICATION NUMBER: US/09/394,272
 ; CURRENT FILING DATE: 1999-09-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 1068
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; US-09-394-272-8

Query Match 10.5%; Score 444; DB 4; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 6.3e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY	234	GDTAGHVLMIHLLDIIQAPDPSTLEKFLGRIPMI-----FNVVVSPHGYE- 281
Db	141	GTITIGEL-----APVETTKKFKQRFNSDLTWSSDDNKKKLYIVLIVSHGLVR 188
QY	282	GQANVLGL-PTGGQIVYILDQVRALENEMVLKKGGLDVP---KILIVTRLI--PD- 334
Db	189	GENMELGRSDTGGQVKYVVELARA-----MSMPGVYRVDLFTQVSSPDV 235
QY	335	-----AKGTSNORLERISGTQHTYILRVPRNENGILKKWISRFDPVPLTF 383
Db	236	DWSYGSPTMLCAGSDGCMGSGG---AYIVRIPC---GPRDKYLKKEALWPYLQEF 288
QY	384	ADDAAGEI-----AAELQGT-----PDFIIGNYSDGNLIVASLLSYKMGITOCNIAHALE 432
Db	289	VGCALAHILMSKALGEQVNGRPVLYVTHGYADAGVAAALLSGALNVPMVLTGHSLG 348
QY	433	KTK-----YPDSDFMKNFDEKHFSCQFTADIAMNADFIITSTQEIAGSKNTVGQYE 488
Db	349	RNKLEQLLKQGRMSKEEIDSTYKIMRRIEGEELALDASELIVITSTQEID-----EQW- 401
QY	489	SHTAFTPLGLYRVVHGIDV-----DGFVVKLEKVLARARRGVSGHGRYMRVVPVPGMDFSNVVVH-- 448
Db	402	-----GLY-----DGFVVKLEKVLARARRGVSGHGRYMRVVPVPGMDFSNVVVH-- 448
QY	530	KAKRLTSLHGSITENLYDPEQNDHEIG-----HLDERSKPIILFSMAR 571
Db	449	-----EDIDGDDGVKDDIVGLEGASPKSMPTIWAETVWRFLTNPHKPMILALS 496
QY	572	LDRVKNITGLVEAFKAKLRELNVLVVAGYNDVKNKSDREIEAEIKMHKILKTHNLF 631
Db	497	PDPKNITTLVKAFCGRPLRELANTLIMGNRDDIDDMASAGNASVLTTLVKLIDKYDLY 556
QY	632	GQPRWLSAQTNRARNCELRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTATLHGGP 691
Db	557	GSVAF-PKHNNQADVPEIYKLAAMKGVFINPALVEFFGLTIEAAAHGLPIVATKNGGP 615
QY	692	AEIIEHGVSGFHIDPYHPEQAVNLMAFFDRCQKDPDHWNVNISGAGLQRIYEKYITWKIYS 751
Db	616	VDITNALNGLLVDPHDQ-----NAIADALKLVADKNLMQECRRNGLRNIH-LYSWPEHC 670
QY	752	ERLMT-LAGVYGFWKVYKSLERLETREYLE 780
Db	671	RTYLTRVAGC-----RLRNPRLWK 689

RESULT 14
 US-08-553-436A-6
 ; Sequence 6, Application US/08553436A
 ; Patent No. 5866790
 ; GENERAL INFORMATION:
 ; APPLICANT: HESSE, Holger
 ; APPLICANT: MULLER-ROBER, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

```

Qy 639 AQTNRANGELYRYIADTHGAFVOPALYEAFGLTWEMNTGCLPTFATLHGGPAZLIEHG 599
Db 548 KHHKQADVPEIYRLAAKTGVIINPAFIEPFGTLTIEAAHGLPMVATKNGGPFVDIQRYL 607
Qy 699 VSGFHDPVHPEQAV-----NLMA D--PFDRCKODECHWVNISGAGLRIYEKYTWKIYS 751
Db 608 DNGLLVDP-HEQOQSIATALLKLVDKQIWTCKQON-----GLKNIH-LYSWPEHS 655
Qy 752 ERLMT 756
Db 656 KTYLS 660

RESULT 15
US-09-394-272-7
; Sequence 7, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 7
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Beta vulgaris
; US-09-394-272-7

Query Match 10.5%; Score 441.5; DB 4; Length: 1045;
Best Local Similarity 26.8%; Pred. No. 1e-31;
Matches 146; Conservative 102; Mismatches 190; Indels 107; Gaps 24

Qy 272 VVVVSPHGYF-GQANVLGL-PDTGGQIVYILDQVRALENE-----MVLRLKKQGLDV 321
Db 163 LVLIISLHLIRGENMELGRSDTGGQVKYVVVELARALGSGMPGVYRVLDLITQVSSPDVDM 222

```

QY	322	S	----	PKLILVTRLI2PAKGTSCNQRLEISGTOHTYTLRVPFRNEMGILKKWISFRPDP	370
Db	223	SYGEPTMMLNPR	----	DSNGFDDDD--DEMGSAGVIIRPFI-----GPRDKYIAKEBLWP	273
QY	379	YLETFAEDAAGEIA	-----	AELQGT-----PDFIIGNYDGNILVASLLSYOM3ITQCN	427
Db	274	YIPEFVDGALNHIVQMSKVLGEQIGSGETVPVAIHGHYADAGSAAALLSGENVPMLLT	333	----	
QY	428	AHALEKTKY2D	-----	SDIFWNKFDKYHPSQOFTADIILAMNADFIILSTYGEIA	478
Db	334	GHSIGLRDKLEQLLKQGRMSKDDI	-----	NNTYKIMRRIEABEELSLOASEITVIITSTROEIE	389
QY	479	GSKNTVGQYESHTAFTLPGI	-----	YRVVHGIDV---FDPKFNIVSPGADMSYFFPHTEK	530
Db	389	-----	EQHLYDGFDPVLERKLARMKGGVSCYGRFMRVMVIPPOMEFNHIVPH	438	----
QY	531	AKELTSLHSGIENLIYDPEQNDEH	-----	IGHLDDRSKPIFLFMAERLDRVKNI	578
Db	439	-----	EGMDG--BTEETEEHPTSPDPPIWAEITMRPFSPKPKMILALARPDPKKN	488	----
QY	579	TGLVEAFKAKLRELNLNVVAGYDNDVNSKDBEEIABIEKOMHEILKTHNGOFQFWIS	638	----	
Db	489	TTIVKAFGFCRPRELANLTILINGNRDGDIDEMSTSSSVLLSVILKIDQYDLGXQVAY-P	547	----	
QY	639	AQTNRRNSELRYIADTHGAFQOPALYEAFGLTVVVEAMTCGLPTFATLHGGAETIEHG	698	----	
Db	548	KHHQADVFETIYLAAKTKGVFINPAFIEPFGILTLEAAAHGLPMWATONGPVDIQRLV	607	----	
QY	699	VSGFHIDPYHPBOAV	-----	NLMAD--FFDRCQKDDPDHWNVINSAGLQRIYEKVTWKIYS	751
Db	608	DNCELLYDP--HEOOSIATALLKVLADKQMTFKCOON	-----	GLNKIIEHJYSWPEHS	655

QY 752 ERLMT 756
: :
Db 656 KYLS 660

Search completed: May 24, 2004, 11:28:51
Job time : 22.4153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 53,2675 Seconds

(without alignments)
4254.056 Million cell updates/sec

Title: US-10-080-114a-2

Perfect score: 4217

Sequence: 1 STHAGSRVDTLHARNEL.....YILKRELAKTVLAIDPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4217	100.0	802	5	Aae28499 Corn suc
2	4177	99.1	809	5	Aae28502 Corn Sus3
3	3456	82.0	809	5	Rbb92810 Herbicida
4	3158	74.9	766	2	Aar66222 Sucrose-s
5	3126	74.1	797	6	Abr39586 A. thalia
6	3105.5	73.6	805	5	Abb93752 Herbicida
7	3105.5	73.6	805	6	Abr39585 A. thalia
8	3049.5	72.3	773	5	Aae28503 Maize suc
9	2993.5	71.0	802	5	Aae28500 Corn suc
10	2990.5	70.9	808	3	Aay85664 Rice suc
11	2985	70.8	816	5	Aae28501 Corn suc
12	2974	70.5	816	7	Adc07856 Rice prot
13	2974	70.5	816	7	Adc08209 Rice prot
14	2964.5	70.3	815	7	Adc68460 Lolium pe
15	2961	70.2	806	5	Aau97898 Cotton su
16	2960	70.2	814	7	Adc68366 Lolium pe
17	2934	69.6	816	7	Adc68367 S. arundi
18	2924.5	69.4	808	7	Adc68459 Lolium pe
19	2920.5	69.3	808	7	Adc68364 Lolium pe
20	2916.5	69.2	808	5	Abg69063 Amino aci
21	2914.5	69.1	771	3	Aay85666 PS3 prot
22	2906.5	68.9	808	7	Adc68365 S. arundi
23	2904.5	68.9	808	5	Abb92501 Herbicida
24	2879.5	68.3	805	3	Aab16282 Eucalyptu
25	2879.5	68.3	805	3	Aab16336 Eucalyptu

ALIGNMENTS

RESULT 1

Aae28499
ID AAE28499 standard; protein; 802 AA.

XX AC AAE28499;

XX DT 27-DEC-2002 (first entry)

XX DE Corn sucrose synthase (Sus3).

XX KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
cellulose; corn; Sus3.

XX OS Zea mays.

XX PN WO200267662-A1.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-US005137.

XX PR 22-FEB-2001; 2001US-0270777P.

XX (PION-) PIONEER HI-BRED INT INC.

XX PI Dhugga KS, Helentjaris TG, Niu X;

XX DR WPI; 2002-691625/74.

XX N-PSDB; RAD45849.

XX PT New polynucleotide and its encoded sucrose synthase, useful for
modulating the level of sucrose synthase in transgenic plants (e.g. maize
or soybean) to improve stalk length, reduce grain breakage, or improving
plant or grain strength.

XX PS Claim 12; Page 103-104; 125pp; English.

XX CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
constitutive sucrose synthase (Sus1) and their corresponding nucleic
acids. The polynucleotide, or its encoded protein, is useful for
modulating the level of sucrose synthase in a transgenic plant.
XX CC increasing cellulose production in the stalk tissue of a transgenic
plant, or increasing the concentration of cellulose in the tissues of a
seed of a transgenic plant. This is particularly useful in plant (e.g.
maize or soybean) breeding, especially for e.g. improving stalk length in
maize, reducing grain breakage during combining, transport or movement
into storage, or improving plant or grain strength. The present sequence

Aab28141 Sucrose s
Aau80753 Eucalyptu
Abb93562 Herbicida
Adc08297 Rice prot
Adc07858 Rice prot
Abb91573 Herbicida
Adc07862 Rice prot
Abb93633 Herbicida
Adc07860 Rice prot
Adc07854 Rice prot
Aaw53103 Arabaena
Abg69054 Amino aci
Aab16313 Pinus rad
Abg69052 Amino aci
Aab16309 Eucalyptu
Aab16312 Pinus rad
Aay85667 Plant col
Aab16284 Pinus rad
Abm73686 DNA clone
Aab16314 Pinus rad

26 2879.5 68.3 805 3 AAB28141
27 2879.5 68.3 805 5 AAU80759
28 2867.5 68.0 808 5 ABB93562
29 2755.5 65.3 777 7 ADC08297
30 2755.5 65.3 777 7 ADC07858
31 2340.5 55.5 942 5 ABB91573
32 2319.5 55.0 786 7 ADC07862
33 2296 54.4 843 5 ABB93633
34 2248.5 53.3 798 7 ADC07860
35 1971 46.7 514 7 ADC07854
36 1833 43.5 806 2 AAW53103
37 1692.5 40.1 395 5 ABG69054
38 1212 28.7 348 3 AAB16313
39 802.5 19.0 225 5 ABG69052
40 709 16.8 149 3 AAB16309
41 635 15.1 217 3 AAB16312
42 623 14.8 198 3 AAY85667
43 622 14.7 158 3 AAB16284
44 615 14.6 204 7 ABM73686
45 587 13.9 139 3 AAB16314


```
CC is corn Sus3 protein
XX Sequence 832 AA;
SQ

Query Match 100.0%; Score 4217; DB 5; Length 802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 802; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STHASGRVEDTLHAHRELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEQPF 60
Db 1 STHASGRVEDTLHAHRELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEQPF 60
QY 61 LQVLSAQAIPLPPVAVAPRPGVWEYRVNVHLSVEQLTVSEYLRFEKELVDGQH 120
Db 61 LQVLSAQAIPLPPVAVAPRPGVWEYRVNVHLSVEQLTVSEYLRFEKELVDGQH 120
QY 121 NDPVYLELDFEPENSVPRNRSSTGNGVQFLNRHLSSTIMFRNRDCLPDLDFLRGHRH 180
Db 121 NDPVYLELDFEPENSVPRNRSSTGNGVQFLNRHLSSTIMFRNRDCLPDLDFLRGHRH 180
QY 181 KGHVMMNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKQFQWGLEKKGWDTAGHV 240
Db 181 KGHVMMNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKQFQWGLEKKGWDTAGHV 240
QY 241 LEMIHLLDIIQAPDPSTLEKFLGRIPMIFNVVVSPHGYEGQANVLGLPDTGQIYVIL 300
Db 241 LEMIHLLDIIQAPDPSTLEKFLGRIPMIFNVVVSPHGYEGQANVLGLPDTGQIYVIL 300
QY 301 DQVRALENEMWLRLKKQGLDVSPKILIVTRLIPDAKGTSCNQRLERISGTQHTYILRVFP 360
Db 301 DQVRALENEMWLRLKKQGLDVSPKILIVTRLIPDAKGTSCNQRLERISGTQHTYILRVFP 360
QY 361 RNENGLIKKWI SFDPWVPLETFAEDAAGEIAAELQTPDFIIGNYSDGNLVASLLSYKM 420
Db 361 RNENGLIKKWI SFDPWVPLETFAEDAAGEIAAELQTPDFIIGNYSDGNLVASLLSYKM 420
QY 421 GITQCNIAHALEKTKYPSDIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQEIAGS 480
Db 421 GITQCNIAHALEKTKYPSDIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQEIAGS 480
QY 481 KNTVGYESHTAFTPLGLYRVVHSGIDVDPKFNIVSPGADMSIYFPHTEKAKELTSLHGS 540
Db 481 KNTVGYESHTAFTPLGLYRVVHSGIDVDPKFNIVSPGADMSIYFPHTEKAKELTSLHGS 540
QY 541 IENLIYDPEQNDHIGLDDRSKPIILFMSMARLDVRKNITGLVEAPAKAKLRVLNLVYV 600
Db 541 IENLIYDPEQNDHIGLDDRSKPIILFMSMARLDVRKNITGLVEAPAKAKLRVLNLVYV 600
QY 601 AGYNDVNKSKDREIEIAIEKMHLEIKTHNLFGQFRWISAOINARMCGLYRYIADTHGAF 660
Db 601 AGYNDVNKSKDREIEIAIEKMHLEIKTHNLFGQFRWISAOINARMCGLYRYIADTHGAF 660
QY 661 VQPALYEAFLTVVEAMTCGLPTFATLHGSPABIIIEHGVSGFHDIPVHPQAVNLMADPF 720
Db 661 VQPALYEAFLTVVEAMTCGLPTFATLHGSPABIIIEHGVSGFHDIPVHPQAVNLMADPF 720
QY 721 DRCKQDPDHVNI SGAGLQRIYKYTKIYSERLMTLAGVYGFVKYKLERLETRYLE 780
Db 721 DRCKQDPDHVNI SGAGLQRIYKYTKIYSERLMTLAGVYGFVKYKLERLETRYLE 780
QY 781 MFYILKRELAKTVPLAIDQFQ 802
Db 781 MFYILKRELAKTVPLAIDQFQ 802

RESULT 2
AAE28502
XX ID AAE28502 standard; protein; 809 AA.
XX AC AAE28502;
XX DT 29-AUG-2003 (revised)
XX DT 27-DEC-2002 (first entry)
```

Corn Sus3-Sorghum EST chimeric protein.

Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1; transgenic plant; plant breeding; grain breakage; grain strength; enzyme; cellulose; corn; Sus3; chimeric.

Zea mays.

Sorghum propinquum.

Chimeric.

Key Location/Qualifiers

Region 1..13

Region /note= "Sorghum propinquum EST DNA encoded peptide"

Region 14..809

Region /note= "Corn Sus3 protein"

W0200267662-A1.

06-SEP-2002.

21-FEB-2002; 2002WO-06005137.

22-FEB-2001; 2001US-0270777P.

(PIOM-) PIONEER HI-BRED INT INC.

Dhugga KS, Helentjaris TG, Niu X;

WPI; 2002-691625/74.

N-PSDB; AAD45856.

New polynucleotide and its encoded sucrose synthase, useful for modulating the level of sucrose synthase in transgenic plants (e.g. maize or soybean) to improve stalk length, reduce grain breakage, or improving plant or grain strength.

Claim 12; Page 120-121; 125pp; English.

The invention relates to two sucrose synthases, shrunken-1 (Sh1) and constitutive sucrose synthase (Sus1) and their corresponding nucleic acids. The polynucleotide, or its encoded protein, is useful for modulating the level of sucrose synthase in a transgenic plant, increasing cellulose production in the stalk tissue of a transgenic plant, or increasing the concentration of cellulose in the tissues of a seed of a transgenic plant. This is particularly useful in plant (e.g. maize or soybean) breeding, especially for e.g. improving stalk length in maize, reducing grain breakage during combining, transport or movement into storage, or improving plant or grain strength. The present sequence is Corn Sus3-Sorghum EST chimeric protein. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 809 AA;

Query Match 99.1%; Score 4177; DB 5; Length 809;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DRYEDTTHAHRNELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEQFLDVIRS 66

Db 14 DRYEDTTHAHRNELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEQFLDVIRS 73

QY 67 AQEAIPLPPVAVAPRPGVWEYRVNVHLSVEQLTVSEYLRFEKELVDGQNDPVL 126

Db 74 AQEAIPLPPVAVAPRPGVWEYRVNVHLSVEQLTVSEYLRFEKELVDGQNDPVL 133

QY 127 ELDFEPENSVPRNRSSTGNGVQFLNRHLSSTIMFRNRDCLPDLDFLRGHRHGHMM 186

Db 134 ELDFEPENSVPRNRSSTGNGVQFLNRHLSSTIMFRNRDCLPDLDFLRGHRHGHMM 193

QY 187 LNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKQFQWGLEKKGWDTAGHVLEIHL 246

Db 194 LNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKQFQWGLEKKGWDTAGHVLEIHL 253

QY 247 LLDIIQAPDPSSTLEKFLGRIPMFNVVVSPHGYFGQANVLGLPDTGGQIYVILDOVRAL 306
 DB 254 LLDIIQAPDPSSTLEKFLGRIPMFNVVVSPHGYFGQANVLGLPDTGGQIYVILDOVRAL 313
 QY 307 ENEWLRLKKQGLDVSPKILIVRLIPDAKGTSCNORLERISGTQHTYVILRVPPRNENGI 366
 DB 314 ENEWLRLKKQGLDVSPKILIVRLIPDAKGTSCNORLERISGTQHTYVILRVPPRNENGI 373
 QY 367 LKRWISRFVWPYLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITOCN 426
 DB 374 LKRWISRFVWPYLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITOCN 433
 QY 427 IAHALEKTKYDSDIIFWKNFDEKHFSCQFADIIAMNNADFIITSTYQRIAGSKNTVGQ 486
 DB 434 IAHALEKTKYDSDIIFWKNFDEKHFSCQFADIIAMNNADFIITSTYQRIAGSKNTVGQ 493
 QY 487 YESHTAFTLPGLYRVVHGIDVDFDPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSNIENLIY 546
 DB 494 YESHTAFTLPGLYRVVHGIDVDFDPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSNIENLIY 553
 QY 547 DPEQNDHGHLDLDRSKPILFNSMARLDRVKNITGLVEAFAPAKAKRLRELNLVYVAGYNDV 606
 DB 554 DPEQNDHGHLDLDRSKPILFNSMARLDRVKNITGLVEAFAPAKAKRLRELNLVYVAGYNDV 613
 QY 607 NKSQKREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRYIADTHGAFVQPALY 666
 DB 614 NKSQKREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRYIADTHGAFVQPALY 673
 QY 667 EAFGLTVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDYHPEQAVNLMAADFDRCKQD 726
 DB 674 EAFGLTVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDYHPEQAVNLMAADFDRCKQD 733
 QY 727 PDHWNISGAGLQRIYEKTYWIKYISERIMTLAGYVGFWKYVSKLERLETTRYLEMFIYK 786
 DB 734 PDHWNISGAGLQRIYEKTYWIKYISERIMTLAGYVGFWKYVSKLERLETTRYLEMFIYK 793
 QY 787 FRELAKTVPLAIDQPQ 802
 DB 794 FRELAKTVPLAIDQPQ 809

RESULT 3

AB892810

ID AB892810 standard; protein; 809 AA.

AC AB892810;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 2021.

XX Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

XX W0200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP009892.

XX 28-AUG-2001; 2001WO-EP009892.

XX (FARB) BAYER AG.

XX Tietjen K, Weidler M;

XX WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant

organisms.

XX Claim 5; SEQ ID NO 2021; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (AB890790-AB894016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides

XX Sequence 809 AA;

QY Query Match 82.0%; Score 3456; DB 5; Length 809;
 Best Local Similarity 79.9%; Pred. No. 2.2e-305;
 Matches 635; Conservative 89; Mismatches 69; Indels 2; Gaps 1;

QY 7 DRVEDTLHNEHNEVALLSKYVNGKGILOPHHILDALDEVQSG--GRALAEGLFDVL 64
 DB 14 DRVODTLSAHRNELVALLSRVYDQKGILOPHNLIDELESVIGDDETKSLSDGPGEL 73
 QY 65 RSAQEAIVLPFFVAIAVRPFGVMEYVRYVNHLSVEQLTVSEYLRKFEELVGDQNDPY 124
 DB 74 KSAMEAIVPFFVALAVRPPGVMEYVRYVNFELSVEQLTVSEYLRKFEELVGDNSDPF 133
 QY 125 VLELDFPFPNVPRPNRSSIGNGVQFLNHLSSIMPRNRDCLPELDFLGRHKHGV 184
 DB 134 CLELDFFPFNANVRPSPRSSIGNGVQFLNHLSSVMFRNKDCLPELDFLGRHKHGV 193
 QY 185 NMLNDRCISGLRQSLVTKAEHLKLPADTPYSQFAYKFOEWLEKMGWDTAGHLEMI 244
 DB 194 IXLNDRCISGLRQSLVTKAEHLKLPADTPYSQFAYKFOEWLEKMGWDTAGHLEMI 253
 QY 245 HLLDIIQAPDPSSTLEKFLGRIPMFNVVVSPHGYFGQANVLGLPDTGGQIYVILDOVR 304
 DB 254 HLLDIIQAPDPSSTLEKFLGRIPMFNVVVSPHGYFGQANVLGLPDTGGQIYVILDOVR 313
 QY 305 ALENEMVLRKKQGLDVSPKILIVRLIPDAKGTSCNORLERISGTQHTYVILRVPPRNEN 364
 DB 314 ALETEMVLRKKQGLDVSPKILIVRLIPDAKGTSCNORLERISGTQHTYVILRVPPRNEN 373
 QY 365 GILKRWISRFVWPYLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITQ 424
 DB 374 GILKRWISRFVWPYLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITQ 433
 QY 425 CNIAHALEKTKYDSDIIFWKNFDEKHFSCQFADIIAMNNADFIITSTYQRIAGSKNTV 484
 DB 434 CTIAHALEKTKYDSDIIFWKNFDEKHFSCQFADIIAMNNADFIITSTYQRIAGSKNTV 493
 QY 485 GQYESHGAFGLPGLYRVVHGIDVDFDPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSNIENL 544
 DB 494 GQYESHGAFGLPGLYRVVHGIDVDFDPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSNIENL 553
 QY 545 IYDPEQNDHGHLDLDRSKPILFNSMARLDRVKNITGLVEAFAPAKAKRLRELNLVYVAGYNDV 604
 DB 554 IYDPEQNDHGHLDLDRSKPILFNSMARLDRVKNITGLVEAFAPAKAKRLRELNLVYVAGYNDV 613
 QY 605 DVNKSQKREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRYIADTHGAFVQPA 664
 DB 614 DVNKSQKREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRYIADTHGAFVQPA 673
 QY 665 LYRAFGLTVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDYHPEQAVNLMAADFDRCK 724
 DB 674 LYRAFGLTVVEAMTCGLPTFATLHGSPAEIIEHGVSGFHDIDYHPEQAVNLMAADFDRCK 733
 QY 725 QDPDHWNISGAGLQRIYEKTYWIKYISERIMTLAGYVGFWKYVSKLERLETTRYLEMFIY 784
 DB 734 QDPDHWNISGAGLQRIYEKTYWIKYISERIMTLAGYVGFWKYVSKLERLETTRYLEMFIY 793
 QY 785 LKFRRELAKTVPLAID 799

Db 386 TFAEDASNEISAEQLQWPNLIIGNYSDGNLAVASLLASKLGVQCNIAHALEKTKYPESDI 445
 QY 442 FKNFDEKXHFSCQTADIIANNKADFIITSTYQIAGSKNTVGOYESHTAFTLGLYRV 501
 Db 446 YMRNEDKXHFSSQFTADIIANNKADFIITSTYQIAGSKNTVGOYESHTAFTLGLYRV 505
 QY 502 VHGIQVDFPKFNVSPGADMSIYFFPTEKAKRLTSLHGSINLIYDPEQNDHIGHLDDR 561
 Db 506 VHGIQVDFPKFNVSPGADMSIYFFPTEKAKRLTSLHGSINLIYDPEQNDHIGHLDDR 565
 QY 562 SKPIIFSMARLDVRKNITGLVFAKAKAKRLVNLVWVAGYNDVNVKSKDRBEAIEIKM 621
 Db 566 SKPIIFSMARLDVRKNITGLVFAKAKAKRLVNLVWVAGYNDVNVKSKDRBEAIEIKM 625
 QY 622 HELIKTNLFGQPRWISAQTNRANGELYRYIADTHGAFVQALYEAFGLTVVEAMTCGL 681
 Db 626 HSLIEQYDLHGEFRWIAAQNRRANGELYRYIADTHGAFVQALYEAFGLTVVEAMTCGL 685
 QY 682 PTFATLHGGPAEIIHGVSGFHDIPVHPQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 741
 Db 686 PTFATLHGGPAEIIHGVSGFHDIPVHPQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 745
 QY 742 YEKYTKWYSERLLTAGVYAFWKVSKLERLETRRYLEMFLYKPRELAKTVPLAIDQ 800
 Db 746 YERYTKWYSERLLTAGVYAFWKVSKLERLETRRYLEMFLYKPRELAKTVPLAIDQ 804

RESULT 7
 ABR39585
 ID ABR39585 standard; protein; 805 AA.
 AC ABR39585;
 XX ABR39585 (first entry)
 DT 12-JUN-2003
 DE A. thaliana lipid metabolism protein (LMP)-clone ID Pk118.
 KW Lipid metabolism protein; LMP; seed storage; plant; transgenic.
 OS Arabidopsis thaliana.
 XX WO2003014376-A2.
 XX 20-FEB-2003.
 XX 12-AUG-2002; 2002WO-US025586.
 XX 10-AUG-2001; 2001US-0311414P.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Mittendorf V, Haertel H, Cirpus P;
 XX WPI; 2003-256595/25.
 XX N-PSDB; A3276371.
 PT New nucleic acid molecule encoding lipid metabolism protein, useful for
 PT producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.
 XX Claim 2; Fig 12B; 108pp; English.
 CC The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polynucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABR39572-587 represent A. thaliana LMP sequences

XX Sequence 805 AA;
 SQ Query Match 73.6%; Score 3105.5; DB 6; Length 805;
 Best Local Similarity 74.3%; Fred. No. 2e-273; Indels 5; Gaps 3;
 Matches 579; Conservative 97; Mismatches 98;
 QY 24 LSKYNKKGILQPHILDA-LDEYQSGG-RALARGPFLDLRSQAQEAIVLPFPAIAV 81
 Db 29 LVRYVAQGGILQSHQILDEELKTVKVDGTLEDLANKSPFKVL--QEAIVLPFPAIAV 85
 QY 82 RRRPGVWEYRVNVNHELSSVEQLTVSSYLPKBEELVDGQNDPVLELDEPEFNVSPRPN 141
 Db 86 RRRPGVWEYRVNVNHELSSVEQLTVSSYLPKBEELVDGQNDPVLELDEPEFNVSPRPN 145
 QY 142 RSSISGNGVOELNRHLSSIMERNRDLPLDPLRGRHKGHVMLNDRISQSLGRQSVL 201
 Db 146 RSSISGNGVOELNRHLSSIMERNRDLPLDPLRGRHKGHVMLNDRISQSLGRQSVL 205
 QY 202 TKAEEHLSKLPADTPYSOFAYKQEMGLEKMGDGTAGHVLMTLHLLDIIQAPDPSTLEK 261
 Db 206 ARAEEFLSKLPATPYSEFEFELQSGMFERGWDGTAKVSEMVHLLDIIQAPDPSTLEK 265
 QY 262 FLGRIPMIENVVSPHGFQANVLGLDGTGQIVYILDQVRALENEMVLRKKOGLDV 321
 Db 266 FLGRIPMIENVVSPHGFQANVLGLDGTGQIVYILDQVRALENEMVLRKKOGLDV 325
 QY 322 SPKLLIVTLIPDAKGTSCNORLERISGTQHTYILRVPPERNNGILKKMISRFDVPWYLE 381
 Db 326 IPKLLIVTLIPDAKGTSCNORLERISGTQHTYILRVPPERNNGILKKMISRFDVPWYLE 385
 QY 382 TFAEDAGHIAAELOQTDPFIIGNYSNGNLVSLASYKMGITOCNTAHALEKTKYPESDI 441
 Db 386 TFAEDASNEISAEQLQWPNLIIGNYSDGNLAVASLLASKLGVQCNIAHALEKTKYPESDI 445
 QY 442 FKNFDEKXHFSCQTADIIANNKADFIITSTYQIAGSKNTVGOYESHTAFTLGLYRV 501
 Db 446 YMRNEDKXHFSSQFTADIIANNKADFIITSTYQIAGSKNTVGOYESHTAFTLGLYRV 505
 QY 502 VHGIQVDFPKFNVSPGADMSIYFFPTEKAKRLTSLHGSINLIYDPEQNDHIGHLDDR 561
 Db 506 VHGIQVDFPKFNVSPGADMSIYFFPTEKAKRLTSLHGSINLIYDPEQNDHIGHLDDR 565
 QY 562 SKPIIFSMARLDVRKNITGLVFAKAKAKRLVNLVWVAGYNDVNVKSKDRBEAIEIKM 621
 Db 566 SKPIIFSMARLDVRKNITGLVFAKAKAKRLVNLVWVAGYNDVNVKSKDRBEAIEIKM 625
 QY 622 HELIKTNLFGQPRWISAQTNRANGELYRYIADTHGAFVQALYEAFGLTVVEAMTCGL 681
 Db 626 HSLIEQYDLHGEFRWIAAQNRRANGELYRYIADTHGAFVQALYEAFGLTVVEAMTCGL 685
 QY 682 PTFATLHGGPAEIIHGVSGFHDIPVHPQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 741
 Db 686 PTFATLHGGPAEIIHGVSGFHDIPVHPQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 745
 QY 742 YEKYTKWYSERLLTAGVYAFWKVSKLERLETRRYLEMFLYKPRELAKTVPLAIDQ 800
 Db 746 YERYTKWYSERLLTAGVYAFWKVSKLERLETRRYLEMFLYKPRELAKTVPLAIDQ 804

RESULT 8
 AAE28503
 ID AAE28503 standard; protein; 773 AA.
 XX AAE28503;
 AC AAE28503;
 XX AAE28503 (first entry)
 DT 27-DEC-2002
 DE Maize sucrose synthase consensus protein.
 XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 XX cellulose; maize.

Db 421 AHKLGVTQCTIAHALEKTKYNSDIYLDKEDSQVHPSQCTADLIAMNHTDFTIITSTFQE 480
 QY 477 IAGSKNTVGQYESHATATLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEAKRLTS 536
 Db 481 IAGSKDVTGQYESHIAFTLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEAKRLTA 540
 QY 537 LHGSIENLIYDPEONDEHIGHLDRSKPILFSPMARLDRVKNITGLVEAFKAKRLRLVM 596
 Db 541 FHEPIEELLYSEVENDKFKVLKDKNPIIFSMARLDRVKNITGLVEMYGKAHLRLAN 600
 QY 597 LVVAGVNDVNKSKDRBEIAIEKQHELIKTHNLI FGQFRWISAGTNRARNGLYRYIADT 656
 Db 601 LVIWCG-DHGNQSKDRBEQABFKQWGLIDQYKLGHRWISAGTNRARNGLYRYICDT 659
 QY 657 HGAFVQALYEAFLTVEAMTGLPTFATLHGGAPELIEHGVSGPHLDVPHPEQAVNLM 716
 Db 660 KGVFVQAFYEAFLTVEAMTGLPTIATCHGGGAPELII VGVSGELHDPVHSDKAADIL 719
 QY 717 ADFFDRCKQDPDHWNVNISGAGLQRIYBKTYWKIYSERLMTLAGVYGVKYSKLERLETR 776
 Db 720 VNFEKCKQDSTYWDNISQGLQRIYBKTYWKIYSERLMTLAGVYGVKYSKLERLETR 779
 QY 777 RYLEMFYILKRELAKTVPLAID 799
 Db 780 RYTEMFYALKYRSLASAVPLAID 802

RESULT 11
 ID AAE28501 standard; protein; 816 AA.
 AC AAE28501;
 DT 27-DEC-2002 (first entry)
 XX Corn sucrose synthase (Sus1).
 KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 KM transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 KN cellulose; corn; chromosome 9.
 XX Zea mays.
 OS
 PN WC200267662-A1.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005137.
 XX
 PR 22-FEB-2001; 2001US-0270777P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Dhugga KS, Kelentjaris TG, Niu X;
 XX
 DR WPI; 2002-631625/74.
 DR N-PSDB; AAD45852.
 XX
 XX New polynucleotide and its encoded sucrose synthase, useful for
 PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
 PT or soybean) to improve stalk length, reduce grain breakage, or improving
 PT plant or grain strength.
 XX
 XX Example 9; Page 114-115; 125pp; English.
 PS
 CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
 CC acids. The polynucleotide, or its encoded protein, is useful for
 CC modulating the level of sucrose synthase in a transgenic plant.
 CC increasing cellulose production in the stalk tissue of a transgenic
 CC plant, or increasing the concentration of cellulose in the tissues of a
 CC seed of a transgenic plant. This is particularly useful in plant (e.g.
 CC maize or soybean) breeding, especially for e.g. improving stalk length in

CC maize, reducing grain breakage during combining, transport or movement
 CC into storage, or improving plant or grain strength. The present sequence
 CC is corn Sus1 protein. Corn Sus1 gene is located at chromosome 9
 XX
 SQ Sequence 816 AA;
 Query Match 70.8%; Score 2985; DB 5; Length 816;
 Best Local Similarity 69.8%; Pred. No. 1.9e-262;
 Matches 559; Conservative 106; Mismatches 128; Indels 8; Gaps 3;
 QY 3 HASGDRVEDTTHAHRNELVALLSKYVNGKGILOPHHIL----DALDEVQSGGGRALAPG 58
 Db 14 HSVRERIGDSLSEHNELVAVFTRLKNLKGKMLQPHQIIAEVYNAIPEAE---REKLKDG 70
 QY 59 PFLDVLASQAIAVLPPVATAVPRPGVWVYVNVNHELSEVQLTYSYLRFKELVDG 118
 Db 71 AFEDVLRAAQAIVIPPWVALAIRPGVGVYVNVNSELAVEELRVPEYLFQFKQLVEE 130
 QY 119 QHNDPVYVLELDFEPFNVSVPNPNSSISGNGVQFLNRHLSSIMERNRDCLEPLIDFLRGH 178
 Db 131 GPNNFVLELDFEPFNASFPNPSLSKSGVQFLNRHLSSKLFHDKESMYPLNLAH 190
 QY 179 RHKGHVWMLNDRIOSLGRLOSVLTKABEHLKSLPADTPYSQFAYKQFQWGLEKMGDTPAG 238
 Db 191 NYKGMTWMLNDRIKRSLSALQALRKABEHLSTLQADTPYSEFHRFQELGLEKMGDCAK 250
 QY 239 HVLEMIHLILDIICAPQPESTLEKELGRIPMFNVVNVSPHGYEQANVLGPDGQIVY 298
 Db 251 RAQETIHLDDLLEAPDESTLEKELGTIPMFNVVNVILSPHGYFAQANVLGPDGQGVY 310
 QY 299 ILDOVRALENEMWLRLKQGLDVSPKILIVTRLIPDAKGTSCNORLERISGTQHYILRV 358
 Db 311 ILDOVRAMENEMLLRIKQGLDITEKILIVTRLIPDATGTTCCGQLEKVLGTEHCHILRV 370
 QY 359 PFRNENGLIKWISRFVDMVYLETFAEDAAGEIAAEALQGTDPDTIGNYSDGNLVALSLY 418
 Db 371 PFRTEINGIVRWISRFVDMVYLETYTDVAHEIAGELQANPDLIIGNYSDGNLVALCLAH 430
 QY 419 KMGITQCNIAHALEKTKYPSDIEKNPDEKXHFSCQPTADIIAMNADFLITSTVOEIA 478
 Db 431 KMGVTHCTIAHALEKTKYPSDLYKXFFEDHYFSCQPTTDLIAMNADFLITSTFQIEA 490
 QY 479 GSKNTVGQYESHATFTPLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEAKRLTSLH 538
 Db 491 GNKDTVGQYESHMAFTWGLYRVVHGIDVDFPKFNIVSPGADLSIYFPHTEAKRLTSLH 550
 QY 539 GSIENLIYDPEONDEHIGHLDRSKPILFSPMARLDRVKNITGLVEAFKAKRLRLVM 598
 Db 551 PEIBELLYSQENTEHKFLVNDNRNKPFIIFSMARLDRVKNITGLVEYGRNKLRLQELVNLV 610
 QY 599 VVAGVNDVNKSKDRBEIAIEKQHELIKTHNLI FGQFRWISAGTNRARNGLYRYIADTHG 658
 Db 611 VVCG-DHGNPNSKDRBEQABFKQWGLIDQYKLGHRWISAGTNRARNGLYRYICTDTRG 669
 QY 659 AFVQALYEAFLTVEAMTGLPTFATLHGGAPELIEHGVSGPHLDVPHPEQAVNLMAD 718
 Db 670 AFVQAFYEAFLTVEAMTGLPTFATYAGPAELIWHVSGYHIDPYQGDKASALLVD 729
 QY 719 PFDRCQDPPDHWNVNISGAGLQRIYBKTYWKIYSERLMTLAGVYGVKYSKLERLETR 778
 Db 730 PFDRCQAPSHNSKISQGLQRIEIKYTWKLYSERLMTLAGVYGVKYSKLERLETR 789
 QY 779 LEMFYILKRELAKTVPLAID 799
 Db 790 LEMLYALKYRTMASTVPLAVE 810

RESULT 12
 ADC07856
 ID ADC07856 standard; protein; 816 AA.
 XX
 AC ADC07856;
 XX

DT 18-DEC-2003 (first entry)
 XX Rice protein sequence Seq ID122 related to grain filling.
 DE
 XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 XX WO2003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002WO-1B002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX
 XX WPI; 2003-229341/22.
 DR N-PSDB; ADC07855.
 XX
 XX New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 FT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 XX Claim 1; SEQ ID NO 122; 130pp; English.
 XX
 XX This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences.
 XX
 XX Sequence 816 AA;
 XX
 XX Query Match 70.5%; Score 2974; DB 7; Length 816;
 XX Best Local Similarity 69.8%; Pred. No. 2e-261;
 XX Matches 557; Conservative 105; Mismatches 134; Indels 2; Gaps 2;
 XX
 QY 3 HASGDVEDTHAHNELVALLSKYVNGKGLIQPHILDALDEVQSGGR-ALAEQPL 61
 DB 14 HSVREIGSLSAHNELVAVFTRLVNKGMLQAHQIIAEYNNASREAREKLKGAFE 73
 QY 62 DVLRSQAELVLPFPFAIAVRPGVWVYRVNVNHELVSFQLTVSEYLRKEELVDQHN 121
 DB 74 DVLRSQAEGIVISFWALATRPFGWYRVNVNSELAVELLTVPEYVQKEQIVEGTN 133
 QY 122 DPVLELDFPPNVSPVRNRSSIGNGVQFLNRHLSSIMFRNDCLEPLDLFLGRHRK 181
 DB 134 NNFVLELDFPPNASFPPSLSKSIGNGVQFLNRHLSSKLFPHDKESMYPLNFLRAHNYK 193
 QY 182 GHVWMLNDRISQSLGRISLVLTAKAEHLKSKLPADTPYSQPAYKTFQEWLEKMGDGTAGHVL 241
 DB 194 GXTTMLNDRISLSALQALRKAEHLKSLGSLADTPYSEPHRTQELGLEKMGDCAKRSQ 253

QY 242 SMHLLDLIIQADPSPLEKPLGRIPMIENWVWVSPHGYGQANVIGLPTDGGQIVYLD 301
 DB 254 ETHLLDLLEADPSPLEKPLGRIPMIENWVWVSPHGYGQANVIGLPTDGGQIVYLD 313
 QY 302 QVRALENEMVLRKXQGLDVSPKLIIVTRLLIPDAKGTSCNQRLEISQGTQRTYILRVFPR 361
 DB 314 QVRAMENEMLRKXQGLDVSPKLIIVTRLLIPDAKGTSCNQRLEISQGTQRTYILRVFPR 373
 QY 362 NENGILKXWISREDVWPYLETFADDAAGETAELQGTDFPIIGNYSDGNLVASLLSYKMG 421
 DB 374 TENGIVKXWISREDVWPYLETFADDAAGETAELQGTDFPIIGNYSDGNLVASLLSYKMG 433
 QY 422 ITQCNIAHALEKTKYKPSDIFPKWDFEKYHFSQFTADIIAMNNADFLITSTYOEIAGSK 481
 DB 434 VTHTCIAHALEKTKYKPSDIFPKWDFEKYHFSQFTADIIAMNNADFLITSTYOEIAGSK 493
 QY 482 NTVGQYESHVAFPLPGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLPSIHGSI 541
 DB 494 DTVGQYESHVAFPLPGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLPSIHGSI 553
 QY 542 ENLIYDPEQNDHLHLDKRSKPILESMARLDKVNITGLVEAFKAKLRELVNLYVVA 601
 DB 554 EELLYSEVDNNEHFKMLKDRNKPIIFSMARLDKVNITGLVEAFKAKLRELVNLYVVA 613
 QY 602 GYNDVNSKDRKEETAEKEMHELIKTNLFGQPRWISAQTNRAENGELXYIADTHGAFV 661
 DB 614 G-DHGNPSKDKESQAEFKKMFOLIEQYNLNGHFWISAQNNRVNGELXYICTKGAFF 672
 QY 662 QPALYEAFLTVVEMTCGLPTFATLHGGPABIEHGVSGPHIDPHYHPEQAVNLMAFPD 721
 DB 673 QPAFYEAFLTVVEMTCGLPTFATLHGGPABIEHGVSGPHIDPHYHPEQAVNLMAFPD 732
 QY 722 RCKQDPDHVNISSAGLQRIYKXKLYKXERLMTLAGVYGFVKYKSLERLETRVLEW 781
 DB 733 KCQEDPSHWTKISQGGLORIEYKXKLYKXERLMTLAGVYGFVKYKSLERLETRVLEW 792
 QY 782 FYILKRFELAKTVPLAID 799
 DB 793 LYALKYRTMASTVPLAVE 810
 XX
 XX ADC08209 standard; protein; 816 AA.
 AC ADC08209;
 XX
 XX 18-DEC-2003 (first entry)
 XX
 XX Rice protein sequence Seq ID514 related to grain filling.
 XX
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 XX WO2003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002WO-1B002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI

PI Glazebrook J, Katagiri F, Kreps J, Provart N, Rieke D;

XX WP2; 2003-229341/22.

DR N-PSDB; ADC08208.

XX

PT New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.

PS Claim 34; SEQ ID NO 514; 130pp; English.

XX

XX This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences.

XX Sequence 816 AA;

Query Match 70.5%; Score 2974; DB 7; Length 816;

Best Local Similarity 69.8%; Pred. No. 2e-261;

Matches 557; Conservative 105; Mismatches 134; Indels 2; Gaps 2;

QY 3 HASGRVETTHAHRNELVALLSKVYKKGKGLQPHILDALDEVGSGR-ALAEGRFL 61

DB 14 HSRERIGDSAHNELVAVTRLVNLGKMLQAHQIIAEYNNATSEADREKLKDGAFE 73

QY 62 DVLRSAQAIPLPPFAIVRPRPGVWEYVRNVHLSVEQLTVSEYLFKEELVDGQHN 121

DB 74 DVLRSAQGVIVSPVALAIRPRPGVWEYVRNVSELAVELITVPEYLFQKQLVEEGRN 133

QY 122 DPVTVLEDPFPPNVSPVPRNRS:GNGVQFLNRHLSIMFRNDCLEPLDLFLGRHRK 181

DB 134 NNFWVLEDPFPPNVSPVPRNRS:GNGVQFLNRHLSIMFRNDCLEPLDLFLGRHRK 193

QY 182 GHVMMNDRIQSLGRLQSVLTAEHLKSLPADTPYSQFAYKPEMGLEKGGDRAGVL 241

DB 194 GMTMLNDRIRSLALQGLARXAEHLGSLADTPYSEFHRFPQELGLEKGGDCAKRSQ 253

QY 242 EMHLLDIIQAPDPSLEKFLGRIPMIENVVSPHGVFGQANVLGLPDTGQIVVILD 301

DB 254 ETIHLLEDLEAPDPSLEKFLGTPWVENVVIMSPHGYPAQANVLGYDPTGGQVYILD 313

QY 302 QVRALENMVLKXQGLDVSPKILIVTRILIPAKGTSCNQLERISGTQTYILRVPR 361

DB 314 QVRAMENMLRIKQGLMITPRILIVTRLLPDATGTTGQRLKVLGTETHILRVPR 373

QY 362 NENGILKXWISFDVWPYLETAEADAAGIAELQTPPIIGNYSYDGNLVSLLSYKNG 421

DB 374 TENGIVRWISRFVWPYLETETDVAHEIAGELQANPOLIITGNSYDGNLVSLLAHKNG 433

QY 422 ITQCNIAHALETKYKPDSDIFWKNFDEKHFSCQPTADIIAMNADPILITSTVQETAGSK 481

DB 434 VTHCTIAHALETKYKPNSDLYKKFEDYHFSQPTTDIIAMNADPILITSTVQETAGSK 493

QY 482 NTVGQVESHTAFTPLGXYRVHVGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLHSGI 541

DB 494 DTWGQVESHTAFTPLGXYRVHVGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLHSGI 553

QY 542 ENLIYDPEQNDHGHLDLDRKPIILFMAALDRVKNITGLVFAPAKCAKRLNVLVVA 601

DB 554 EELLYSEVDNNEHFKMLKORNPPIIFSMARLDVRVKNLTGLVELYGRNPRLOELNVLVVC 613

QY 602 GYNDVNVKSKORBEIAIEIKMHKLIKTHNLFGOPRWISAOINRARNGBELRYVIADTHGAFV 661

DB 614 G-DHGNPSSKDEBQAEFKKGFLLISQYNLNGHRIWISAQNRVRNGBELRYVICDTGAFV 672

QY 662 QPALYEAFLGTLTVVEAMTGLPTPATLHGGPAETIEHGVSGFHIDPYHPEQAVNLMADFFD 721

DB 673 QPAFYEAFLGTLTVVESMTGCLPTFATAYGPAEIIIVNGVSGFHIDPYGDKASALLEVEFE 732

QY 722 RCKQDDPHWNISGAGLQRIYKYTWKYSERLMTLAGYGVFWKYVSKLRLERTRRYLEM 781

DB 733 KQODESHWTKISQGGLORIEIKYTWKYSERLMTLAGYGVFWKYVSKLRLERTRRYLEM 792

QY 782 FYILKRELAKTVPLAID 799

DB 793 LYALKRTWASTVPLAVE 810

RESULT 14

ADC68460

ID ADC68460 standard; protein; 815 AA.

XX ADC68460;

XX 18-DRC-2003 (first entry)

XX Lolium perenne fructan biosynthesis protein SEQ ID NO:170.

XX Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;

XX biosynthetic pathway; plant.

XX Lolium perenne.

XX WO2003040306-A2.

XX 15-MAY-2003.

XX 07-NOV-2002; 2002WO-NZ000239.

XX 07-NOV-2001; 2001US-0337703P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (WRIGHT-) WRIGHTSON SEEDS LTD.

XX Demmer J, Forster RL, Gibson JB, Shenk MA, Norriss MG, Glenn M;

XX Saulsbury KM, Hall C;

XX MPI; 2003-441544/41.

XX N-PSDB; ADC68424.

XX New polynucleotide encoding polypeptides from Lolium perenne or Festuca

XX arundinacea, useful for modulating the biosynthesis of lignin, fructan or

XX tannin in a plant.

XX Claim 18; SEQ ID NO 170; 240pp; English.

XX The present invention describes isolated polynucleotides (I) encoding

XX proteins (II) from Lolium perenne and Festuca arundinacea which are

XX active in lignin, fructan and tannin biosynthetic pathways. Also

XX described: (1) an isolated oligonucleotide probe or primer comprising at

XX least 10 contiguous residues complementary to 10 contiguous residues of

XX (I); (2) a kit comprising the oligonucleotide probe or primer; (3) a

XX genetic construct comprising (I); (4) a transgenic plant cell comprising

XX the genetic construct of (3); (5) a plant or its seed, fruit or progeny

XX comprising the transgenic plant cell of (4); (6) modulating one or more

XX of the lignin, fructan or tannin compositions of a plant; (7) producing a

XX plant having one or more of the lignin, fructan or tannin compositions;

XX and (8) modifying the activity of (II) involved in a lignin, fructan or

XX tannin biosynthetic pathway in a plant. (I) can be used for modulating

XX the biosynthesis of lignin, fructan or tannin in a plant. The present

XX sequence is used in the exemplification of the present invention.

XX Sequence 815 AA;

XX SQ

Query Match	70.3%;	Score 2964.5;	DB 7;	Length 815;
Best Local Similarity	69.0%;	Pred. No. 1.4e-260;	Indels 9;	Gaps 4;
Matches 553;	Conservative 112;	Mismatches 127;	Indels 9;	Gaps 4;
QY	3	HASGDRVEDTLHAHRELVALLSKYVKNKGKILQPHHIL----	DALDEVQSGGRALAE	58
DB	14	HSVRERIGDSLSAHPNELVAVFTRVLNGLKGMQLQHILAEYNTAIPAE-	--REKLKDG	70
QY	59	PFLDLVRSQAQEAIVLPFVAIAVRPQGWYVRYVNHLSVQLTVSEYLRKELVDC	118	
DB	71	AFEDVLRQAQEAIVISFWALAIRPQGWYVRYVNHLSVQLTVSEYLRKELVDC	130	
QY	119	QHNDPVVLELDFPFFNVSPRPNRSSISNGVQFLNRHLSIMFRNRDCLPDLRCH	178	
DB	131	SNKD--FVLELDFPFFNVSPRPNRSSISNGVQFLNRHLSIMFRNRDCLPDLRCH	199	
QY	179	RHKGHVNLNDRIOSTGRQSVLTAKAEHLISKLPADTPYSQPAKYQEWGLEKMGWGTAG	238	
DB	190	NYKGMPMNDRVRSLSALQALRKAEHLISGLPADTPYSDPHRFQELGLEKMGWGTAG	249	
QY	239	HVLEMLHLLDITQADPSTLEKFLGRIPIFNVVSVPHGYQANVLGLPDTGGIVY	298	
DB	250	RAQETHLLDLEADPSTLEKFLGRIPIFNVVSVPHGYQANVLGLPDTGGIVY	309	
QY	299	ILDQVRALENEMVRLKKQGLDVSFKILIVTRILPQAKGTSQNRLEISGTHQVILRV	358	
DB	310	ILDQVRALENEMVRLKKQGLDVSFKILIVTRILPQAKGTSQNRLEISGTHQVILRV	369	
QY	359	PRFNENGILKKWISRFVWPYLETFPAEDAAGEITAELOQTPDPIIGNYSGNIVASLLSY	418	
DB	370	PRFNENGILKKWISRFVWPYLETFPAEDAAGEITAELOQTPDPIIGNYSGNIVASLLSY	429	
QY	419	KMGITCOTNAHALEKTKYPSDILFWNEDEKHYFSCQFTADITAMNADPIITSTQELA	478	
DB	430	KMGITCOTNAHALEKTKYPSDILFWNEDEKHYFSCQFTADITAMNADPIITSTQELA	489	
QY	479	GSKNTVQZESHFTAFPLGLYRVHGVDFDPKFNIVSPGADMSIYFPFTEKAKRLTSLH	538	
DB	490	GSKNTVQZESHFTAFPLGLYRVHGVDFDPKFNIVSPGADMSIYFPFTEKAKRLTSLH	549	
QY	539	GSINLIYDQENDEHGHLDKSKPILFSMARLDVKNITGLVEAPAKCAKURELVNLY	598	
DB	550	PEEELLYSDVDNDEHGFVKDKRNPFIISMARLDVKNITGLVEAPAKCAKURELVNLY	609	
QY	599	VVAGYVNVNKSQDREIAETKMHLEIKTHLFGQFRLWISQOTNRANGELYIADTHG	658	
DB	610	VVAGYVNVNKSQDREIAETKMHLEIKTHLFGQFRLWISQOTNRANGELYIADTHG	668	
QY	659	AFVQPALEYAFLTVVEAMTCGLPTFATLHGGPABEIIHGVSGFHIDPHYEPQAVNLAD	718	
DB	669	AFVQPALEYAFLTVVEAMTCGLPTFATLHGGPABEIIHGVSGFHIDPHYEPQAVNLAD	728	
QY	719	FDRCKQDQDHNWISGAGLQRIYKTKIYSERLMTLAGVYGFYKYSKLERETRY	778	
DB	729	FDRCKQDQDHNWISGAGLQRIYKTKIYSERLMTLAGVYGFYKYSKLERETRY	788	
QY	779	LEFYILKPRELAKTVPLAID 799		
DB	789	LEFYILKPRELAKTVPLAID 809		
RESULT 15				
ID	AAU97898			
AC	AAU97898;			
XX	13-AUG-2002 (first entry)			
DT	Cotton sucrose synthase SuSy protein.			
DE	Cotton; Sucrose synthase; Susy; fibre; seed; transgenic; plant; enzyme.			
XX				
KW				
XX				

OS	Gossypium hirsutum.			
XX	Key	Location/Qualifiers		
FT	Misc-difference 414	/label= Unknown		
FT		/note= "Encoded by NAC"		
XX	W0200245485-A1.			
XX	13-JUN-2002.			
XX	07-DEC-2001; 2001WO-AUG01580.			
XX	08-DEC-2000; 2000AU-00001975.			
XX	08-DEC-2000; 2000US-0251852P.			
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.			
XX	Llwelllyn D, Furbank R, Ruan Y;			
XX	WPL; 2002-463779/49.			
XX	N-PSDB; ABK52880.			
XX	Altering fibre development or properties of a fibre producing plant by modulating sucrose synthase activity and/or expression in such plants, useful for enhancing fibre yield and quality and for increasing seed size.			
XX	Claim 5; Page 57-60; 62pp; English.			
XX	This invention relates to a novel method for altering fibre development or properties of a fibre producing plant by modulating sucrose synthase (SuSy) activity and/or expression in such plants. The invention also comprises a fibre producing plant comprising a chimaeric gene in its genome, the seeds of the plant and fibre isolated from the plant. The method is useful for altering fibre development or properties of a fibre producing plant like cotton plant. Therefore, the method is useful for enhancing fibre yield, enhancing fibre quality and for increasing seed size in a fibre producing plant. The present sequence represents the cotton sucrose synthase (SuSy) protein used to create the transgenic plant of the invention			
XX	Sequence 806 AA;			
QY	Query Match	70.2%;	Score 2961;	DB 5; Length 806;
DB	Best Local Similarity	69.7%;	Pred. No. 2.9e-260;	Indels 2; Gaps 2;
DB	Matches 555;	Conservative 112;	Mismatches 127;	Indels 2; Gaps 2;
QY	3	HASGDRVEDTLHAHRELVALLSKYVKNKGKILQPHHILDEVQSGGRALAE	62	
DB	10	HSURERLDETLAHRNEILLALLSRIEKGKILQHQHILFEFAIPENKKLGAFF	69	
QY	63	VLRSAQEAIVLPFVAIAVRPQGWYVRYVNHLSVQLTVSEYLRKELVDC	122	
DB	70	VLRSAQEAIVLPFVAIAVRPQGWYVRYVNHLSVQLTVSEYLRKELVDC	129	
QY	123	PVLELDFPFFNVSPRPNRSSISNGVQFLNRHLSIMFRNRDCLPDLRCH	182	
DB	130	NFVLELDFPFFNVSPRPNRSSISNGVQFLNRHLSIMFRNRDCLPDLRCH	189	
QY	183	HVNLNDRIOSTGRQSVLTAKAEHLISKLPADTPYSQPAKYQEWGLEKMGWGTAG	242	
DB	190	KNMNLNDRIOSTGRQSVLTAKAEHLISKLPADTPYSQPAKYQEWGLEKMGWGTAG	249	
QY	243	MHLLDITQADPSTLEKFLGRIPIFNVVSVPHGYQANVLGLPDTGGIVVILQ	302	
DB	250	MIQLLDLEADPSTLEKFLGRIPIFNVVSVPHGYQANVLGLPDTGGIVVILQ	309	
QY	303	VRALENEMVRLKKQGLDVSFKILIVTRILPQAKGTSQNRLEISGTHQVILRV	362	
DB	310	VRALENEMVRLKKQGLDVSFKILIVTRILPQAKGTSQNRLEISGTHQVILRV	369	
QY	363	ENGILKKWISRFVWPYLETFPAEDAAGEITAELOQTPDPIIGNYSGNIVASLLSY	421	

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 15:32:41 ; Search time 4542.4 seconds
(without alignments)
17993.23c Million cell updates/sec

Title: US-10-080-114A-1

Perfect score: 2737

Sequence: 1 gtcacccacgctccggcg.....aaaaaaagggcgccgc 2737

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_vrt:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2644.2	96.6	2705	11	AY104856
2	1165.2	42.6	3056	13	BU103683
3	1151	42.1	3140	11	AY103630
4	794.6	29.0	1005	13	BQ619258

5	793	29.0	938	13	BQ619406
6	722	26.4	835	14	CA280212
7	704.8	25.8	888	14	CB662799
8	702.8	25.7	909	14	CB629313
9	688.6	25.2	841	14	CB648550
10	684.6	25.0	886	14	CB628458
11	676.2	24.7	745	14	CD426853
12	676	24.7	836	14	CB631982
13	664	24.3	690	14	CD442316
14	655.6	24.0	808	14	CB651486
15	654.2	23.9	817	14	CB666247
16	647.6	23.7	797	14	CB647500
17	643.2	23.5	801	14	CB641607
18	637.2	23.3	727	13	CA066428
19	636.8	23.3	824	14	CB68706
20	636.8	23.3	860	14	CB627276
21	636.2	23.2	785	14	CB677314
22	634	23.2	802	14	CB633383
23	625.2	22.8	812	14	CB663333
24	623.6	22.8	807	14	CB633104
25	622	22.7	767	14	CB682789
26	620	22.7	804	14	CB627329
27	618.8	22.6	806	14	CB627200
28	615.8	22.5	836	14	CB635134
29	615.2	22.5	832	14	CB648734
30	613.6	22.4	839	14	CB645387
31	611.6	22.3	803	14	CB647961
32	610.6	22.3	833	14	CB631361
33	610.2	22.3	836	14	CB631302
34	607.8	22.2	779	14	CB635859
35	609.2	22.0	651	14	CF632182
36	599.2	21.9	800	14	CB628700
37	594	21.7	700	14	CA195492
38	593.2	21.7	787	14	CB629315
39	592.8	21.7	756	14	CB628904
40	580.6	21.2	763	14	CB673208
41	570.2	20.8	763	14	CB628938
42	560.6	20.5	727	14	CB632976
43	560	20.5	720	14	CA196779
44	545.4	19.9	628	14	CA283716
45	541.6	19.8	951	14	CF514627

ALIGNMENTS

RESULT 1
AY104856
LOCUS
DEFINITION Zea mays PC0079420 mRNA sequence.
ACCESSION AY104856
VERSION AY104856.1 GI:21207934
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 2705)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

JOURNAL Unpublished (2002)

REFERENCE 2 (bases 1 to 2705)

Coe,E.H.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

source
 .. 2705
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:634420"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 96.6%; Score 2644.2; DB 11; Length 2705;
 Best Local Similarity 99.1%; Pred. No. 2.2e-311;
 Matches 2669; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

18 GCGACCGGTCGAGACACCCCTCCACGGGCAACGAGGCTCGTGGCCCTCCCTGTCCA 77
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 1 GCGACCGGTCGAGACACCCCTCCACGGGCAACGAGGCTCGTGGCCCTCCCTGTCCA 60
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 78 AGTACGTGAACAAGGGGAAGGCACTCTCAGCCGACCAACATCTCGACGGCTCGAGC 137
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 61 AGTACGTGAACAAGGGGAAGGCACTCTCAGCCGACCAACATCTCGACGGCTCGAGC 120
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 138 AGGTCCAGGGCTCCGGGGCGCGGCTAGCCGAGGGACCTTCTCGAGCTCCTCCGCT 197
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 738 TCCTTCTAGACATCATTCAGGCGCCAGACCCATCTACCTTAGAGAAATCTTGGGGAGGA 797
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Db 721 TCCTTCTAGACATCATTCAGAGCCGACAGCCCATCTACACTAGAGAAATCTTGGGAGGA 780
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QY	1878	AGACCAACCTGTTGGGCGGAGTTCGGCTGGATCTCTGCCAGACAAACAGGCGCGTA	1937
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QY	1938	ACGGGAGCTCTATCGCTACATCGCTGATACCCATGCTGTTTCGTCACGCGGCTTGT	1997
Db	1921	ACGGGAGCTCTATCGCTACATCGCTGATACCCATGCTGTTTCGTCACGCGGCTTGT	1980
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 ORGANISM
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 1 (bases 1 to 3056)
 Nogueira, F.T.S., de Rosa, V.E. Jr., Menossi, M., Ulian, E.C. and
 AUTHORS

Attuda, P.	
RNA expression profiles and data mining of sugarcane response to	
low temperature	
Plant Physiol. 132 (4), 1811-1824 (2003)	
22795309	
PUBMED	
12913139	
Contact: Nogueira PTS	
Bioinformatics Lab	
Organization for Nucleotide Sequencing and Analysis	
C.P. 6176, Campinas, SP 13083-970, Brazil	
Tel: 55 19 37881101	
Fax: 55 19 37881089	
Email: tebalduenicamp.br.	
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REFERENCE 1 (bases 1 to 3140)
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 3140)
 Coe, E.H.
 REFERENCE Direct Submission:
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 JOURNAL If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Malbot, Stanford or Pat
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    1 (bases 1 to 938)
  Wang, H. and Bohner, H.J.
  Genomics of plant stress tolerance
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  Contact: Mark Fredricksen
  Department of Plant Biology
  University of Illinois
  1201 W. Gregory Dr., Urbana, IL 61801, USA
  Tel: 2172655473
  Email: bohnerlab@life.uiuc.edu.
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DB 552 CTACCTCTGAGATGTTCTACATACATGAGTTCGCGAGCTGCGGAGACCGTGGCTTGC 611
QY 2392 AATTCACCAACCGCAGTAGCTTGGCGCACTGCGCACTGCGTACGACTTGGTACAGACTGA 2451
DB 612 AATTCACCAACCGCAGTAGCTTGGCGCACTGCGTACGACTTGGTACAGACTGA 671
QY 2452 AACCTGAGAGGACCTTCAGTAATTTAGGCGCGCAGACGCTAGCCAAATAAATGTGCCGA 2511
DB 672 AACCTGAGAGGACCTTCAGTAATTTAGGCGCGCAGACGCTAGCCAAATAAATGTGCCGA 731
QY 2512 GCTGCACTGCTTTTATATATATATATATATATATATATATATATATATATATATATAT 2571
DB 732 GCTGCACTGCTTTTATATATATATATATATATATATATATATATATATATATATATAT 791
QY 2572 GGGTT---GCAGTTGTGTGTTCTGTTTACTTGT---ATTGCTCAAGCTGTCGGCT 2625
DB 792 GGGTTGTGAGTGTGTGTTCTGTTTACTTGT---ATTGCTCAAGCTGTCGGCT 851
QY 2626 GCAATTTTCTTTGCTGCGAGCGCGCAGGCGCTGGTG-AAAGTCTGATAAATACATCATAT 2683
DB 852 GCAATTTTCTTTGCTGCGAGCGCGCAGGCGCTGGTG-AAAGTCTGATAAATACATCATAT 911
QY 2684 TCT-GTTCACCTGTGCAAAAAA 2709
DB 912 TCTGTTGACCTGTGAAAAA 938

RESULT 6
CA280212
LOCUS
DEFINITION
  SCVPLB2C05C09.g LB2 Saccharum officinarum cDNA clone SCVPLB2C05C09
  5', mRNA sequence.
ACCESSION
  CA280212
VERSION
  CA280212.1 GI:36007504
KEYWORDS
  EST.
SOURCE
  Saccharum officinarum
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Saccharum.
    1 (bases 1 to 835)
  Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
  The libraries that made SUCEST
  Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
  Contact: Arruda P
  Centro de Biologia Molecular e Engenharia Genetica
  Universidade Estadual de Campinas
  Caixa Postal 6070, 13083-970, Campinas SP, Brazil
  Tel: 55 19 3788 1137
  Fax: 55 19 3788 1089
  Email: parruda@unicamp.br
  Clone distribution: clone distribution information can be found
  through the Brazilian Clone Collection Center (BCCC) at
  http://www.bccc.net.br
  Plate: C05 row: C column: 09
  Seq primer: T7 Promoter Primer.
FEATURES
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    /mol_type="mRNA"
    /db_xref="taxon:4547"
    /clone="SCVPLB2C05C09"
    /lab_host="DH10B"
    /clone_lib="LB2"
    /note="Organ: Lateral buds from plants adult plants
  
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growing in greenhouse; Vector: pSport1; Site 1: Sali;
Site 2: Not1; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucet.lad.ic.unicamp.br/public>

OR-GIN

Query Match 26.4%; Score 722; DB 14; Length 835;
Best Local Similarity 92.5%; Pred. No. 2.3e-78;
Matches 769; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 761 CGAGCCATCTACCTAGAGAAATTTCTGGGAGAGATCCCATGATTTTAACTGTTGT 820
DB 1 CGAGCCCATCAACCTTAGAGAAATTTCTGGGAGAGATCCCATGATTTTAACTGTTGT 60
QY 821 GTGGTATCCCTCATGTGATCTTTGGTCAAGCTAAATGTTAGCTTGGCCAGACACAGGA 880
DB 61 GTGGTATCCCTCATGTGATCTTTGGTCAAGCTAAATGTTAGCTTGGCCAGACACAGGA 120
QY 881 GGCAGATCGTCTATATCTAGGACCAAGTCCGTCACCTAGAAAATGAGATGGTCTCCGT 940
DB 121 GGCAGATCGTCTATATCTAGGACCAAGTCCGTCACCTAGAAAATGAGATGGTCTCCGT 180
QY 941 TTAAGAAACAAGGCTTGATGTTTCCCAAGATCTTCAATGTTACTCGGCTGATACCA 1000
DB 181 TTAAGAAACAAGGCTTGATGTTTCCCAAGATCTTCAATGTTACTCGGCTGATACCA 240
QY 1001 GATGCAAAAGACATCATCATGATGAGCGCTTGGAGAAATGAGTGAACACACAGCATACT 1060
DB 241 GATGCAAAAGACATCATGATGAGCGCTTGGAGAAATGAGTGAACACACAGCATACT 300
QY 1061 TACATATTAAGAGTCCCTTACAGAAATGAAAATGGGATCTTAAAGAAATGGATATCAAGA 1120
DB 301 TACATATTAAGAGTCCCTTACAGAAATGAAAATGGGATCTTAAAGAAATGGATATCAAGA 360
QY 1121 TTTGATGTGGCCATCTGGAACATTTGCTGAGGATCTGCTGGTGAATTCGTCT 1180
DB 361 TTTGATGTGGCCATCTGGAACATTTGCTGAGGATCTGCTGGTGAATTCGTCT 420
QY 1181 GAATTACAAGTACTCCAGACTTCAATATGGAACCTACAGTATGAAATCTTGGCG 1240
DB 421 GAATTACAAGTACTCCAGACTTCAATATGGAACCTACAGTATGAAATCTTGGCG 480
QY 1241 TCATGCTATCTTACAGATGGAAATTAACAGTGAACATTCCTCATGCTCTGGAAG 1300
DB 481 TCATGCTATCTTACAGATGGAAATTAACAGTGAACATTCCTCATGCTCTGGAAG 540
QY 1301 ACTAAGTATCCAGATTCAGACATATTTGGAAGATTTGATGAGAGTACCATTTCTCC 1360
DB 541 ACTAAGTATCCAGATTCAGACATATTTGGAAGATTTGATGAGAGTACCATTTCTCC 600
QY 1361 TGGCAGTTCACCTGATATAATTTGCTATGAACAATGCTGATTTATCATCACCAGCA 1420
DB 601 TGTGCTTCACTGCTGATATAATTTGCTATGAACAATGCTGATTTATCATCACCAGCA 660
QY 1421 TACCAAGAAATTCG-TGGAAGCAAAATATCTGTTGGACAGTATGAGAGTCAATCTGCTT 1479
DB 661 TACCAAGAAATTCGTTGGAAGCAAAATATCTGTTGGACAGTATGAGAGTCAATCTGCTT 720
QY 1480 TACTCTGCTGCTGTGACAGCTGACATGTCATGATGGATGATGCTTCCATCCAAAGTTCAA 1539
DB 721 TACTCTGCTGCTGTGACAGCTGACATGTCATGATGGATGATGCTTCCATCCAAAGTTCAA 780
QY 1540 TATAGTCTCTCTGGAGCTGACATGTCATGATGGATGATGCTTCCATCCAAAGTTCAA 1590
DB 781 AATAAACCTCTTGAACCTGGAGGCTGATATATTTTCTTTTACCCCAA 831

RESULT 7
CB662799
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB662799 888 bp mRNA linear EST 09-APR-2003
OSJNEd07C12.f OSJNEd Oryza sativa (japocica cultivar-group) CDNA
clone OSJNEd07C12 5', mRNA sequence.
CB662799
CB662799.1 GI:29666524
EST.

Oryza sativa (japocica cultivar-group)

Oryza sativa (japocica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 888)

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: gta aaa cga cgg cca gtcg

BACKWARD: gga aac agc tat gac cat g

Plate: 07 row: C column: 12

Seq primer: gta aaa cga cgg cca gtcg.

Location/Qualifiers

1..888

/organism="Oryza sativa (japocica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEd07C12"

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/dev_stage="3 week"

/lab_host="DH10B"

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XhoI; 24 hrs after inoculation with Rice Blast (C924C-1)"

ORIGIN

Query Match 25.3%; Score 704.8; DB 14; Length 888;
Best Local Similarity 87.8%; Pred. No. 2.8e-76;
Matches 780; Conservative 0; Mismatches 107; Indels 1; Gaps 1;
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DB 1 GAAGGTTGGGGCGACACAGCTGGATATGCTTGGAGATGATACATCTCTCTGGATG 60
QY 751 CATTCAGGCGCCAGACCCATCTACCCCTAGAGAAATTTCTGGGAGGATCCCATGATTT 810
DB 61 GCTTCAAGCGCTGATCCATCTACTCTTGAGACGTTCTTGGGAAGGATCCCATGATCT 120
QY 811 TAACGTTGTGCTGATCCCTCATGATCTTGGTCAAGCTAATGATAGCTTGGCTGCC 870
DB 121 TAATGTCGTGATGTCCTCATGATATTTTGGCCAAAGCAATGTTGGGCTTACC 180
QY 871 AGACACAGGAGGACAGATCGTCTATATCTATCTGACCAAGTCCGTCGACATAGAAATGAGAT 930
DB 181 AGATCTGGAGGCGAGATGCTATATCTATCTGACCAAGTCCGTCGATGAGATGAGAT 240
QY 931 GGTTCCTCGTTTAAAGAAACAAGGCTTGAATTTTCCCAAGATTCATGTTACTGTCG 990
DB 241 GGTTCCTAGGTTAAAGAAACAAGGCTTGAATTTTACCCCTAAAATTTCTTATGTTACTG 300
QY 991 GCTGATACCAAGTGCAAAAGGACATCATGCAATCAGCGCTTGGAGAAATTAGTGAAC 1050

Db 301 GCTGATACCAGAAGCAAAAGGACATCATGCAATCAGCGTCTTGAGAGATAAGTGGGAC 360
Qy 1051 ACAGCATACTTACATATTAAGAGTCCCTTCGAAATGAAATGSGNTACTTAAAGAAATG 1110
Db 361 ACAACATACTTACATATTAAGAGTCCCTTCGAAATGAAATGSGNTACTTAAAGAAATG 420
Qy 1111 GATATCAAGATTGATGTGGCCATATCTCGAAACATTTGCTGAGGATGCTGCTGCTGA 1170
Db 421 GATATCAAGATTGATGTGGCCATATCTCGAAACATTTGCTGAGGATGCTGCTGCTGA 480
Qy 1171 AATTGCTGCTGAATTAACAGGTACTTCCAGACTTCATAATTTGAAATCTACAGTATGAGAA 1230
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Qy 1231 TCTTGTGCGTCAATGCTTATCTTACAGATGGGAATTCACAGTCCAGATGCTCATGTC 1290
Db 541 TCTTGTGCTCATGCTTATCTTACAGATGGGAATTCACAGTCCAGATGCTCATGTC 600
Qy 1291 TCTGAAAGAACTAAGTATCCAGATTCCAGACATATTTTGGAGAAATTTCCGATGAGAATGA 1350
Db 601 TTTGGAAAGAACTAATATCCAGCTCAGACATATCTGACGAAATGACGATGAGAATGA 660
Qy 1351 CCATTCTCTGCGAGTTCATGCGATATATATGCTATGAAACAACTGCTGATTTTATCAT 1410
Db 661 CCATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 1411 CACCAGACATACCAGAAATTTGCTGGAAGCAAAATCTGCTGACAGTATGAGAGTCA 1470
Db 721 CACCAGACATACCAGAAATTTGCTGGAAGCAAAATCTGCTGACAGTATGAGAGTCA 780
Qy 1471 TACTGCTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529
Db 781 TACTGCTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 1530 CAAAGTTCAATATAGTCTCTCTGAGAGTCAATGCTCAATATCTTTC 1577
Db 841 CAAAGTTCAATATAGTCTCTCTGAGAGTCAATGCTCAATATCTTTC 888

RESULT 8

LOCUS CB629313
DEFINITION OSIIIEB05H07.f OSIIIEB Oryza sativa (indica cultivar-group) cDNA
clone OSIIIEB05H07 5', mRNA sequence.
ACCESSION CB629313
VERSION CB629313.1 GI:29624302
KEYWORDS ESR.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Rhartoideae; Oryzeae; Oryza.
1 (bases 1 to 909)

REFERENCE

AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: H column: 07
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
source 1. .909

/organism="Oryza sativa (indica cultivar-group)"
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/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIIIEB05H07"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIIEB"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

ORIGIN

Query Match 25.7%; Score 702.8; DB 14; Length 909;
Best Local Similarity 86.9%; Pred. No. 4.8e-76;
Matches 773; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Qy 402 ATGCTCAGTCCAGCCCAATCGTCATCATCTATTGGMAACGCTGTCAGTTCCTCA 461
Db 19 ATGCTCAGTCCAGCCCAATCGTCATCATCTATTGGMAACGCTGTCAGTTCCTCA 78
Qy 462 ACGACACTTGTCTCAATCATGTTCCGCAACAGGGAATGCTTGGAGCCCTGTTGGATT 521
Db 79 ACAGGCACTTGTCTCGATCATGTTCCGAAACAGGGAATGCTTGGAGCCCTGTTGGATT 138
Qy 522 TCCTCGTGGCCACCGGCACAGGCGCATGTTATGATGCTTAAATGATAGAAATCAAGCT 581
Db 139 TCCTTCGTGGGCATCGGCATAGGGTCTATGATGCTAAATGACAGGATACAGATC 198
Qy 582 TGGGAGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCCTGTCGAAGAGTGGG 701
Db 199 TGGGAGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCCTGTCGAAGAGTGGG 258
Qy 642 ACACACCATCTCAATTTGCTTATAAAATTTCAAGAGTGGGCGCTCGAGAAAGTGGG 318
Db 259 ACACACCATCTCAAGTTGCTGATATAAGTTTCAAGAAATGGGGAATGGAGAGG 378
Qy 702 GTGATACAGCAGGACATGTTTGGAAATGATCCATCTCTCTAGACATCATTCAGGCGC 761
Db 319 GCGACACAGCTGGATATGCTTGGAGATGATACATCTCTCTCTGATGCTGCAAGCG 821
Qy 762 CAGACCATCTACCTACAGAAATTTCTTGGGAGGATCCCATGATTTTAAAGTGTG 821
Db 379 CTGATCCATCTACTCTTGGAGAGTTCCTTGGGAGGATCCCATGATCTTAAATGCTG 438
Qy 822 TGGTATCCCTCATGATGATCTTGGTCAAGCTTAATGATGATGCTTGGAGTGGAG 881
Db 439 TAGTGTCTCTCATGATATTTGGCCAAAGCAATGTTGGGCTTACCAGATCTGGAG 498
Qy 882 GACAGATGCTATATCTGACCAAGTCCCTGCACTAGAAATGAGATGCTTCTCCGT 941
Db 499 GGCAGATGCTATATCTGACCAAGTCCCTGCACTAGAAATGAGATGCTTCTCCGT 558
Qy 942 TAAAGAAACAGGCTTGTATGTTTCCCAAGATTTCTCATTTGTTACTCGGCTGATACCAG 1001
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Qy 1002 ATGCAAAAGGAACATCATGCAATCAGCGCTTGGAGAAATGATGGAACACAGCATCT 1061
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Qy 1062 ACATATTACGAGTTCCTTCAAGATGGAATGGAATGGAATGGAATGGAATGGAAT 1121
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Db 739 TTGATGTATGCGCTTCTGCGAGAAATTTGCGAGGATGCTGCTGCTGCTGCTGCTGCTG 798
Qy 1182 AATTACAGGTACTTCCAGATCTTCAATTTGGAATCTACAGTATGGAATCTTGTGGCT 1241
Db 799 AACTACAGGTACTTCCAGATCTTCAATTTGGAATCTACAGTATGGAATCTTGTGGCT 858


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QY 1242 CATTGCTATCTTACAGATGGGAAHTTACCAGTGCAGACATTGCTCATGCT 1291
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859 CATTGCTATCTTACAGATGGGAAHTTACCAGTGCAGACATTGCTCATGCT 908

RESULT 9
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LOCUS OSJNEB11P18.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEB11P18 5', mRNA sequence.
ACCESSION CB648550
VERSION CB648550
KEYWORDS EST.
SOURCE CB648550.1 GI:29643543
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 841)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: P column: 18
Seq primer: gta aaa cga cgg cca gtc.

FEATURES
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="OSJNEB11P18"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEB"
/notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

ORIGIN
Query Match 25.2%; Score 688.6; DB 14; Length 841;
Best Local Similarity 88.8%; Pred. No. 2.6e-74;
Matches 745; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 923 AATGAGATGTTCTCCGTTTAAAGAAACAAGGGCTTGATGTTCCCAAGATCTCAT 982
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2 AATGAGATGTTCTTAGTTTAAAGAAACAAGGGCTTGATGTTTACCCCTAAAATCTTTAT 61

QY 983 GTTACTCGGCTGATACCAGATGCAAAAGGAACATCATGCAATCAGCGCTTGAGAGAATT 1042
Db |||||||
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QY 1043 AGTGGAAACAGACATCTTACATATTACAGTTCCTTCAGAAATGAAATGGGATAC 1102
Db |||||||
122 AGTGGAAACAGACATCTTACATATTACAGTTCCTTCAGAAATGAAATGGGATAC 181

QY 1103 AAGAAATGGATATCAAGATTTGATGTGGCCATATCTGGAAACATTTGCTGAGGATGCT 1162
Db |||||||
182 AGGAAATGGATATCAAGATTTGATGTGGCCCTACCTGGGAAATTTGCAGAGGATGCT 241

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QY 1163 GCTGGTGAATTTGCTGCTGAATTAACAAGTACTCCAGACTTTCATATATTTGAAACTACGT 1222
Db |||||||
242 GCTGGTGAATTTGCTGCTGAATTAACAAGTACTCCAGACTTTCATATATTTGAAACTACGT 301

QY 1223 GATGAAATCTTTGTGGCGTCAATTGCTATCTTACAAGATGGAAATCCCAAGTGCACATT 1282
Db |||||||
302 GACGGTAATCTTTGTGTCATCATTTGCTATCTTACAAGATGGAAATCCCAAGTGCACATT 361

QY 1283 GCTCATGCTCTGGAAAGACTAAAGTATCCAGATTCAGACATATTTTGGAGAAATTTCCAT 1342
Db |||||||
362 GCTCATGCTCTGGAAAGACTAAAGTATCCAGATTCAGACATATCTGAGCAAGATGATCAT 421

QY 1343 GAGAATACCAATTTCTCTGCCAGTTTCACTGCTGTATATATTTGCTATGAACAATGCTGAT 1402
Db |||||||
422 GAGAATACCAATTTCTCTGCCAGTTTCACTGCTGTATATATTTGCTATGAACAATGCTGAT 481

QY 1403 TTTATCATCACAGCACATACCAAGAAATTTGCTGGAGCAAAATTAATCTTGGACAGTAT 1462
Db |||||||
482 TTTATTAATCACCAGCACATACCAAGAAATTTGCTGGAGCAAAATTAATCTTGGACAGTAT 541

QY 1463 GAGAGTCATACCTGCTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1522
Db |||||||
542 GAGAGTCATACCTGCTTTACTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601

QY 1523 TTCGATCCAAAGTTCAATATATAGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
Db |||||||
602 TTTGACCCCAAGTTCAACATAGTCTCTCCAGAGCAGACATGCTATATATCTTCCGTCAC 661

QY 1583 ACCGAGAGCCCAAGGAGTCACTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1642
Db |||||||
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QY 1643 CCGGAGCAAAACGATGAACAACATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1702
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QY 1703 TCCATGCGCAAGACTCGACAGCGTGAAGAACATTAACAGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1761
Db |||||||
782 TCCATGCGCAAGACTTGACCGAGTTAAGAACATTAACAGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

RESULT 10
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LOCUS OSIIEB04A18.f OSIIEB Oryza sativa (indica cultivar-group) cDNA
DEFINITION clone OSIIEB04A18 5', mRNA sequence.
ACCESSION CB628458
VERSION CB628458
KEYWORDS EST.
SOURCE CB628458.1 GI:29623447
ORGANISM Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 886)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: A column: 18
Seq primer: gta aaa cga cgg cca gtc.

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Db	781	TGATTTTACCCCTAAATAATCTTTATGTTACTCGGCTGATACCAAGAACAAAGGACATC 840
QY	1018	ATGCAATCAGCGGCTTGAGAGATTAGTGGAAACACAGCATACTTACA 1064
Db	841	ATGCAATCAGCGCTTGTAGAGAA-TAGTGGGACACACATACTTACA 886
RESULT 11		
CD426853		
LOCUS		
DEFINITION	745 bp mRNA linear EST 02-JUN-2003	
ACCESSION	CD426853	
VERSION	CD426853.1	
KEYWORDS	EST	
SOURCE	Sorghum bicolor (sorghum)	
ORGANISM	Sorghum bicolor	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.	
AUTHORS	1 (bases 1 to 745)	
TITLE	Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Eastman, A. and Pratt, L.H.	
JOURNAL	An EST database from Sorghum: salicylic acid-treated seedlings	
COMMENT	Other ESTs: SAI_25_F05.bl_A002 Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu	
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Location/Qualifiers		
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/lab_host="DH10B-T1 phage-resistant E. coli"		
/clone_lib="Salicylic acid-treated seedlings"		
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM salicylic acid (SA). Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."		
ORIGIN		
Query Match	24.7%;	Score 676.2; DB 14; Length 745;
Best Local Similarity	96.0%;	Pred. No. 8.6e-73;
Matches	715;	Conservative 0; Mismatches 28; Indels 2; Gaps 2;
QY	650	TACTCAAAATTTGCTTATAAATTTCAAGAGTGGGCTCGGAGAGGTTGGGTGTATACA 709
Db	1	TACGACAAATTTGCTTATAAATTTCAAGAGTGGGCTCGGAGAGGTTGGGTGTATACA 60

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Location/Qualifiers		
1. .886		
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/db_xref="taxon:39946"		
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/dev_stage="3 week"		
/lab_host="DH10B"		
/clone_lib="OSIIEB"		
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast [PO6-6-3]"		
ORIGIN		
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Best Local Similarity	86.5%;	Pred. No. 7.7e-74;
Matches	767;	Conservative 0; Mismatches 119; Indels 1; Gaps 1;
QY	178	CTTCTCGAGCTCTCGCTCCGCGCAGGAGGCGATCGTCTCGCGCGTTCGTCGCGCAT 237
Db	1	CTTCTCGAGCTCTCGCTCCGCGCAGGAGGCGATCGTCTCGCGCGTTCGTCGCGCAT 60
QY	238	CGCGTGCCTCGCGCGCGCGGAGTTTGGAGTAGTCTCGCGCTCAACGTTCAACGAGTCTAG 297
Db	61	CGCGTGCCTCGCGCGCGCGGAGTTTGGAGTAGTCTCGCGCTCAACGTTCAACGAGTCTAG 120
QY	298	CGTGCAGAGCTCAGAGTCTCGAGTACCTCCGCTTCAAGGAGGAGGTTGTGCAGCGCCA 357
Db	121	CGTGCAGAGCTCAGAGTACCTCCGCTTCAAGGAGGAGGTTGTGCAGCGCCA 180
QY	358	GCACATGATCCCTAGCTTCTCGAGCTTGACITTCGAGCGGCTTCAATGTTCTCAGTCCCAAG 417
Db	181	GCACATGATCCCTAGCTTCTGAGCTTGATTTTGAGCCATTCATGCTCGTTCGAG 240
QY	418	CCCAATCGGTATCATCTATTTGAAACGGTGTGAGTCTCTCAACCGACACTTGTCTC 477
Db	241	CCCAATCGGTATCATCTATTTGAAACGGTGTGAGTCTCTCAACCGACACTTGTCTC 300
QY	478	AATCATGTTCCGCAACAGGAGTTGTTGAGCGCCCTGTTGATTTCTCGTGGCCACCG 537
Db	301	GATCATGTTCCGCAACAGGAGTTGTTGAGCGCCCTGTTGATTTCTCGTGGCCATCG 360
QY	538	GCACAGGGCGATGTATGATGCTTAAATGATAGATACAAAGCTTGGGAGGCTTCAGTC 597
Db	361	GCATAAGGTCATGTCATGATGCTAATGACAGGATACAGAGTCTGGAAGACTTCAGTC 420
QY	598	TGTGCTGACCAAGCTGAGGAGCATTGTCAAGCTCCCTGCTGACACACCATACTCACA 657
Db	421	TGTGCTGACCAAGCTGAGGAGCATTGTCAAGCTCCCACTCCCACTGACACACCATACTCACA 480
QY	658	ATTGCTTATAAATTTCAAGAGTGGGCGCTCGGAGAAAGGTTGGGGTGTATACAGCAGACA 717
Db	481	GTTTCGATATAAGTTTCAGAAATGGGATTTGGAGAGGGTTGGGGGACACAGCTCGATA 540
QY	718	TGTTTGGAAATGATCCATCTCTCTCTAGACATCATTCAGGCGCCAGACCCATCTACCT 777
Db	541	TGTTTGGAGATGATACATCTCTCTCTGATGTGCTGCAAGCGCCTGATCCATCTACTCT 600
QY	778	AGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGTGTGTTGTTGTTGTTGTTGTTGTTG 837
Db	601	TGAGAGCTTCTTGGGAAGGATCCCATGATCTTTAAAGTGTGTTGTTGTTGTTGTTGTTGTTG 660
QY	838	ATACTTTTGTCAAGCTAATGTTATTAGCTTTGCAGACACAGGAGGACAGATGCTCTATAT 897
Db	661	ATATTTTGGCCAAAGCAATGTTGTTGGCTTTACAGATCTGAGGCGCAGATGTTCTATAT 720
QY	898	ACTGACCAAGTCCGTCGACTAGAAAATGAGATGGTTTCTCCGTTTAAAGAAACAAGGGCT 957
Db	721	ACTGACCAAGTCCGTCGACTTGAGAAATGAGATGGTTTCTTGGTTTAAAGAAACAAGGGCT 780
QY	958	TGATGTTTCCCAAGATCTCATCTGTTACTCGGCTGTATACAGATGCAAAAGGACATC 1017

710 GCAGACATGTTTGGAAATGATCCATCTCCTTCTAGACATCAATTCAGCGCCACACCA 769
 Db GCAGACATGTTTGGAAATGATCCATCTCCTTCTAGACATCAATTCAGCGCCACACCA 120
 770 TCTACCCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTTGGGTATCC 829
 Db TCTACCCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTTGGGTATCC 180
 830 CCTCATGATATCTTGGTCAAGCTAATGATTTAGCTTGCAGACACACAGGACACAGATC 889
 Db CCTCATGATATCTTGGTCAAGCTAATGATTTAGCTTGCAGACACACAGGACACAGAT 240
 890 GTCTATATCTAGGACCAAGTCCGTCACCTAGAGAAATGAGATGTTCTCCGTTTAAAGAA 949
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 950 CAGGCTTGTATGTTTCCCAAGATCTCATGTTTACTCGGCTGATACAGATGCAAAA 1009
 Db CAGGCTTGTATGTTTCCCAAGATCTCATGTTTACTCGGCTGATACAGATGCAAAA 360
 1010 GGAACATCATGCAATCAGCGGCTCAGAGAAATGATGGAACACAGCATATCTTACATATTA 1069
 Db GGAACATCATGCAATCAGCGGCTCAGAGAAATGATGGAACACAGCATATCTTACATATTA 420
 1070 CGAGTTCCCTTCAGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 1129
 Db CGAGTTCCCTTCAGAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 480
 1130 TGGCCATATCTGGAACATTTCTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1189
 Db TGGCCATATCTGGAACATTTCTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 1190 GGTACTCCAGACTTCAATTTGGAATCAGTGTGGAATGGAATGGAATGGAATGGAATGGAAT 1249
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 1250 TCTTACAGATGGAAATACCAAGTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1309
 Db TCTTACAGATGGAAATACCAAGTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 1310 CAGATTGACATAT-TTGGAGATTTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1367
 Db CAGATTGACATAT-TTGGAGATTTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 720
 1368 TCAGTCTGATATAATTTGCTATCAA 1392
 Db TCAGTCTGATATAATTTGCTATCAA 745

RESULT 12
 CB631982
 LOCUS
 DEFINITION
 CB631982 836 bp mRNA linear EST 08-APR-2003
 OS:Oryza sativa f. Oryza sativa (indica cultivar-group) cDNA
 clone OS11EB09015 5', mRNA sequence.
 CB631982
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 836)
 Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
 Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
 Large-scale identification of ESTs involved in the interaction
 between rice and Magnaporthe oryzae
 Unpublished (2003)
 CONTACT: Rod Wing
 ARIZONA GENOMICS INSTITUTE
 UNIVERSITY OF ARIZONA
 BIOLOGICAL SCIENCES WEST, 448A, P.O. BOX 210088, TUCSON, AZ
 85721-0088, USA

Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: gta aaa cga cga cga gta
 BACKWARD: gga aac agc tat gac cat g
 Plate: 09 row: 0 column: 15
 Seg primer: gta aaa cga cga gta
 Location/Qualifiers
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 /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
 XhoI; 24 hrs after immunolization with Rice Blast (POB-6-3)"
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 Best local Similarity 88.0%; Pred. No. 8.7e-73;
 Matches 736; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 QY 641 GACACACCATCTACCAATTTGCTTATAAATTTCAAGAGTGGGCTTGGAGAAAGGTTGG 700
 Db 1 GACACACCATCTACCAATTTGCTTATAAATTTCAAGAGTGGGCTTGGAGAAAGGTTGG 60
 QY 701 GGTGATACAGCAGGACATGTTTGGAAATGTCATCTCTTACACATCATTCAGCGG 760
 Db 61 GGGACACACGCTGGATATGTTTGGAGATGATACATCTCTCTGATGCTGCAAGCG 120
 QY 761 CGAGACCATCTACCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGTGT 820
 Db 121 CTTGATCCATCTACTCTTGGAGCTTCTTGGAGAGATCCCATGATCTTAAAGTGT 180
 QY 821 GTGATATCCCTCATGGATATTTTGGTCAAGTAAATGATTTAGGCTTGGCAGACACAGGA 880
 Db 181 GTAGTGTCTCTCATGGATATTTTGGCCAAAGCAATGTTTGGCTTACAGATATCTGA 240
 QY 881 GGAAGATCCCTCATGGATATTTTGGTCAAGTAAATGATTTAGGCTTGGCAGACACAGGA 940
 Db 241 GGGCAGATTTGCTATATATCTGGA CCAAGTCCGTCATTTGGAGATGAGATGTTCTTAGG 300
 QY 941 TTAAGAAACAAGGCTTGTATGTTTCCCAAGATTTCTCATTTGTTACTCGGCTGATACCA 1000
 Db 301 TTAAGAAACAAGGCTTGTATGTTTACCCCTAAATTTCTATTTGTTACTCGGCTGATACCA 360
 QY 1001 GATGCAAAAGGAACATCATGCAATCAGCGCTTGGAGAAATTTAGTGGAAACACAGCATACT 1060
 Db 361 GAAGCAAAAGGAACATCATGCAATCAGCGCTTGGAGAAATTTAGTGGAAACACAGCATACT 420
 QY 1061 TACATATTACAGTCTTCTTCAAGATGAAATGGGATCTTAAAGAAATGATATCAAGA 1120
 Db 421 TACATATTACAGTCTTCTTCAAGATGAAATGGGATCTTAAAGAAATGATATCAAGA 480
 QY 1121 TTTGATGTTGGCCATATCTGGAACAATTTGCTGAGGATGCTGCTGCTGCTGCTGCTGCTGCT 1180
 Db 481 TTTGATGTTGGCCATATCTGGAACAATTTGCTGAGGATGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 1181 GAATTAAGAGTACTCCAGATCTTCAATTTGGAACAATTTAGTGGAAATTTAGTGGAAATTTGCTGCTG 1240
 Db 541 GAATTAAGAGTACTCCAGATCTTCAATTTGGAACAATTTAGTGGAAATTTAGTGGAAATTTGCTGCTG 600
 QY 1241 TCATTGCTATCTTACAGATGGGAATTTACCCAGTGGCAATTTCTCATGCTCTGCTGCTGCTGCTGCTG 1300
 Db 601 TCATTGCTATCTTACAGATGGGAATTTACCCAGTGGCAATTTCTCATGCTCTGCTGCTGCTGCTGCTG 660
 QY 1301 ACTAAGTATCCAGATTCAGACATATTTTGAAGAAATTTCCGATGAGAAATGATACCATTTCTCC 1360

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Db      661 ACTAATATCCAGACTCAGACATATACCTGGAACGATGAGAGTACCATTTCTCC 720
QY      1361 TCCGAGTTTACCTGCTGATATATGCTATGAAACATGCTGATTTTATCATCAGCACA 1420
Db      721 TGTCACTCAGAGCTGATATATGCTGCAATGCAATGCTGATTTTATCATCAGCACA 780
QY      1421 TACCAAGAAATGCTGGAAGCAAAATATCTGTTGGACAGATGAGAGTCACTGTC 1476
Db      781 TACCAGGAATGCTGGCAGCAAAACACAGTTGGACAGTATGAGGCCATATGTC 836

RESULT 13
CD442316 690 bp mRNA linear EST 03-JUN-2003
LOCUS EL01NC407H07.b Endosperm_4 Zea mays cDNA, mRNA sequence.
DEFINITION CD442316
ACCESSION CD442316.1 GI:31357959
VERSION 1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 690);
Mensing, J.
AUTHORS Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
JOURNAL Unpublished (2002)
COMMENT Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.

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source
location/Qualifiers
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/db_xref="taxon:4577"
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/clone_lib="Endosperm 4"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 24.3%; Score 664; DB 14; Length 690;
Best Local Similarity 97.8%; Pred. No. 2.7e-71;
Matches 673; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      898 ACTGGACCAAGTCCTGCTGACTAGAAATGAGATGTTCTCCGTTTAAAGAAACAAGGGCT 957
Db      3 ACAGGCCAAGGGCGTGCCTAGAAAATGAGATGGTTCTTCGTTTAAAGAAACAAGGGCT 62
QY      958 TGAATGTTCCCAAGATCTCATCTGTTACCGCTGATACCAAGTCGAAAGGACATC 1017
Db      63 TGAATGTTCCCAAGATCTCATCTGTTACCGCTGATACCAAGTCGAAAGGACATC 122
QY      1018 ATGCAATCAGCGCTTGAGAGAAATAGTGGAAACACAGCATCTATACATATACGAGTTCC 1077
Db      123 ATGCAATCAGCGCTTGAGAGAAATAGTGGAAACACAGCATCTATACATATGCGAGTTCC 182
QY      1078 CTTTCAAGATGAAATGGGATATCTTAAGAAATGATATCAAGATTTGATGTGGCCATA 1137
Db      183 CTTTCAAGATGAAATGGGATATCTTAAGAAATGATATCAAGATTTGATGTGGCCATA 242
QY      1138 TCTGGAAACATTTGCTGAGCATCTCTGCTGGAATTTGCTGCTCAATTTACAAGTACTCC 1197
Db      243 TCTGGAAACATTTGCTGAGCATCTCTGCTGGAATTTGCTGCTCAATTTACAAGTACTCC 302
QY      1198 AGACTTCATAATTGGAAACTACAGTATGATGGAATCTTTGTGGCGTCAATTGCTATCTTACAA 1257

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Db      303 AGACTTCATATTTGAAACTACAGTATGAAATCTTGTGGCATCTTGTCTATCTTACAA 362
QY      1258 GATGGGAATTCACAGTGCACATTTGCTCATGCTCTGAAAAGACTAAGTATCCAGATTC 1317
Db      363 GATGGGAATTCACAGTGCACATTTGCTCATGCTCTGAAAAGACTAATATCCAGATTC 422
QY      1318 AGACATATTTTGAAGAAATTTGCTGATGAGAGTACCATTTCTCTGCCAGTTCACTGCTGA 1377
Db      423 AGACATATTTTGAAGAAATTTGCTGATGAGAGTACCATTTCTCTGCTGATCTGCTGA 482
QY      1378 TATAATTTGCTATGAACAAATGCTGATTTTATCATCACCAGCACATACCAAGAAATTTGCTGG 1437
Db      483 TATAATTTGCTATGAACAAATGCTGATTTTATCATCACCAGCACATACCAAGAAATTTGCTGG 542
QY      1438 AACCAAAATATCTGTTGGACAGATGAGAGTATCATCTGCTTTTACTGCTGCTGCTGTA 1497
Db      543 AACCAAAATATCTGTTGGACAGATGAGAGTATCATCTGCTTTTACTGCTGCTGCTGTA 602
QY      1498 CCGAGTTGTCATCGGATCGATCTTCGATCCAAAGTTCAATATAGTCTCTCTCTGGAGC 1557
Db      603 CCGAGTTGTCATCGGATCGATCTTCGATCCAAAGTTCAATATAGTCTCTCTCTGGAGC 662
QY      1558 TGACATGTCATATATCTTTCCACATACC 1585
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LOCUS OSJNEB16H11.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEB16H11 5', mRNA sequence.
ACCESSION CB651486
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 808);
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gta g
BACKWARD: gga aac agc tat gac cat g
Plate: 16 row: H column: 11
Seq primer: gta aaa cga cgg cca gta g.
Location/Qualifiers
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XhoI; 24 hrs after inoculation with Rice Blast (Che

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Query Match 24.0%; Score 655.6; DB 14; Length 808;
Best Local Similarity 88.3%; Pred. No. 2.6e-70;
Matches 712; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 671 TTTCAAGAGTGGGGCTGAGAAAGGTTGGGGTGATACAGCAGGACATGTTTTGGAAATG 730
DB 2 TTTCAAGAGTGGGGCTGAGAAAGGTTGGGGTGATACAGCAGGACATGTTTTGGAGATG 61

QY 731 AFCCATCTCTTTAGACATCATTTAGCGCGCAGACCCCATCTACCTAGAGAAATTTCTTG 790
DB 62 AFACATCTCTTTCTGGATGCTTCAAGCGCTGATCCATCTACTCTTGAGAGCTGCTTG 121

QY 791 GGGAGATCCCCATGATTTTAAAGTTGTGTGGTATCCCTCATGGATACTTTGGTCAA 850
DB 122 GGAAGGATCCCCATGATCTTTAATGTCTGTAGTGTCTCTCATGGATATTTGGCCAA 181

QY 851 GCTAATGTATTAGGCTTGCACACACAGCAGGACAGATGCTCTATATCTGACCAAGTC 910
DB 182 GCCAATGTGTGGCTTACCAGATCTGAGGCGGATGTTCTATATCTGACCAAGTC 241

QY 911 CTTGCACTAGAAATGAGATGTTTCCGTTTAAAGAAACAAGGCTTCAATGTTCCCA 970
DB 242 CTTGCAATGGAGATGAGATGTTTCTAGTTTAAAGAAACAAGGCTTCAATTTACCCCT 301

QY 971 AAGATCTCATTTGTTACTCGGCTGATACAGATGCAAGGAGACATCATGCAATCAGCG 1030
DB 302 AAAATCTTATTTGTTACTCGGCTGATACAGAGCAAGGAGACATCATGCAATCAGCG 361

QY 1031 CTTGAGAAATPAGTGGAAACACAGCATCTTACATATTTACGAGTTCCTTTAGAAATGAA 1090
DB 362 CTTGAGAGATPAGTGGGACACACATCTTACATATTTACGAGTTCCTTTAGAAATGAA 421

QY 1091 AATGGATCTTAAAGATGAGATCAAGATTTGATGTTGGCCATATCTGAAACATTT 1150
DB 422 AATGGATCTCAGGAAATGAGATCAAGATTTGATGTTGGCCATATCTGAAACATTT 481

QY 1151 CTTGAGGATGCTGCTGGTGAATTCCTGCTGAATTCAGGCTTACCTCCAGATTTCAAT 1210
DB 482 CAGAGGATGCTGCTGGTGGATTTCTGCAGAACTACCAAGTACTCCAGATTTCAAT 541

QY 1211 GAAATCTACAGTGGAAATCTTTGGGCTCATTTGCTATCTTACAGATGGAAATACC 1270
DB 542 CGAATCTACAGTGAACGTTAACTTTGTTGATCATTTGCTATCTTACAGATGGAAATACC 601

QY 1271 CAGTGAACATTTGCTCATGCTCTGAAAGATCAAGATATCCAGATTCAGACATATTTGG 1330
DB 602 CAGTGAACATTTGCTCATGCTTTGAAAGATCAAGATATCCAGATTCAGACATATTTGG 661

QY 1331 AAGAAATTTGGTGAAGTACCATTTCTCTCCAGTTCACCTGCTGATATATTTGCTATG 1390
DB 662 ACGAGTACAGTGAAGTACCATTTCTCTGTCAGTTCACAGCTGATATATTTGCGCATG 721

QY 1391 AACATGCTGATTTTATCATCACGACATACCAAGAAATTTGCTGGAAGCAAAATACT 1450
DB 722 AACATGCTGATTTTATATATCACGACATACCAAGAAATTTGCTGCGAGCAAAACACA 781

QY 1451 GTTGACAGTATGAGTCAATCTGC 1476
DB 782 GTTGACAGTATGAGGCCATCTGC 807

RESULT 15
CB666247
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DEFINITION
CB666247 OSJNEd13B05.f OSJNEd13B05.5', mRNA sequence.
ACCESSION
CB666247.1
VERSION
CB666247.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
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ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 817)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: B column: 05
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

Query Match 23.9%; Score 654.2; DB 14; Length 817;
Best Local Similarity 88.2%; Pred. No. 3.8e-70;
Matches 724; Conservative 0; Mismatches 93; Indels 4; Gaps 1;

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DB 1 AGAAGCAAAAGGACATCATGCAATCAGCGCTTGAGAGAAATAGTGGACACACATAC 60

QY 1060 TTACATATTTACGATTCCTTCAGAAATGAAATGGATCTTAAGAAATGGATATCAAG 1119
DB 61 TTACATATTTACGATTCCTTCAGAAATGAAATGGATCTTAAGAAATGGATATCAAG 120

QY 1120 ATTTGATGTGGCCATATCTGAAACATTTGCTGAGGATGCTGCTGGTGAATTCCTGC 1179
DB 121 ATTTGATGTATGCTTACCTTACCTGAGAAATTTGACAGGATGCTGCTGGTGGATTCCTGC 180

QY 1180 TGAATTAAGGTACTCTCAGACTTCATATTTGAAACTACAGTATGGAATCTTGTGGC 1239
DB 181 AGAACTACAAGGTACTCTCAGACTTCATATTTGAAACTACAGTATGGAATCTTGTGGC 240

QY 1240 GTCTATGCTATCTTCAAGATGGAAATTTACCCAGTGCACATTTGCTCATGCTGGAATA 1299
DB 241 ATCTATGCTATCTTCAAGATGGAAATTTACCCAGTGCACATTTGCTCATGCTTGAATA 300

QY 1300 GACTAAGTATCCAGATTCAGACATATTTTGGAAATTTTCGATGAGAAGTACCAATTTCTC 1359
DB 301 GACTAATATCCAGATTCAGACATATTTTCGAAAGTACGATGAGAAGTACCAATTTCTC 360

QY 1360 CTGCCAGTTCACTGCTGATATATTTGCTATGAACTGCTGATTTTATCATCACAGCAC 1419
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QY 1420 ATACCAAGAAATTTGCTGGAAGCAAAATACTCTGTCAGACAGTATGAGAGTCACTGCTCT 1479
DB 421 ATACCAAGAAATTTGCTGGAAGCAAAATACTCTGTCAGACAGTATGAGAGTCACTGCTCT 476
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 14:41:46 ; Search time 7059.61 Seconds
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Perfect score: 2757

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Gapop 10.0 , Gapext 1.3

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

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15: em.ba.*

16: em.fun.*

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41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2703.6	98.1	2710	8	AY059416 Zea mays
2	2435.6	88.3	2837	8	AY124703 Zea mays
3	1888	68.5	2716	8	AK099406 Oryza sat
4	1888	68.5	2763	8	AK102158 Oryza sat
5	1809.6	65.6	2412	6	AX653034 Sequence
6	1353.4	49.1	2765	8	AB022091 Citrus un
7	1352.2	49.0	2848	8	AB001071 Pisum sat
8	1316	47.7	2787	8	AB045710 Pyrus pyr
9	1264.8	45.9	2679	8	AY205302 Solanum t
10	1262.8	45.9	2648	8	CPL132000 Craterost
11	1249.8	45.3	2430	6	AX507720 Sequence
12	1249.8	45.3	2506	8	AY142511 Arabidops
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45	1117	40.5	2771	8	AK100306 Oryza sat

ALIGNMENTS

RESULT 1
AY059416
LOCUS 2710 bp mRNA linear PLN 07-NOV-2001
DEFINITION Zea mays sucrose synthase mRNA, partial cds.
ACCESSION AY059416
VERSION AY059416.1 GI:16797784
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2710)
REFERENCE Carlson,S.J., Chourey,P.-S., Helentjaris,T. and Datta,R.
AUTHORS Gene expression studies on developing kernels of maize sucrose
TITLE

Pred. No. is the number of results predicted by chance to have a

synthase (SuSy) mutants show evidence for a third SuSy gene
Plant Mol. Biol. (2001) In press
2 (bases 1 to 2710)
JOURNAL Helentjaris, T.
AUTHORS Direct Submission
TITLE Submitted (10-OCT-2001) Agronomic Traits/TeTD, Pioneer Hi-Bred,
JOURNAL 7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA
FEATURES Location/Qualifiers
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Query Match 98.1%; Score 2703.6; DB 8; Length 2710;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2706; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 98 AGTACGTGAACAAGGGAGAGGAGTCTCTGAGCGCGCAACAATCTCGACGGGCTCGACG 157
DB 61 AGTACGTGAACAAGGGAGAGGAGTCTCTGAGCGCGCAACAATCTCGACGGGCTCGACG 120
QY 158 AGGTCCAGGGCTCGCGGCTCGCGGCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 217
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QY 458 TTGGAAACGGTGTGAGTTTCCTCAACCGGACACTTGTCTCAATCATGTTCGCGCAACAGGG 517
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ORIGIN

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 insert sequence.

AK102158
 AK102158.1 GI:32987367
 FLI CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1

The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team,
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
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 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurokawa, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice

Science 301 (5631), 376-379 (2003)
 2752273
 12869764

2 (bases 1 to 2763)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
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 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.

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 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
 Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica
 rice.
 URL : <http://cdna1.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
 Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
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 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.

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 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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 Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers
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ORIGIN

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 Best Local Similarity 86.0%; Pred. No. 1.4e-306;
 Matches 2092; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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DEFINITION
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
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AUTHORS Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Katagiri,F., Quian,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
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Syngenta Participations AG (CH)
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Db 1901 AGTTCGGTGGATCTCGGCTCAGACGACAGGGCTCGAATGGTGAGCTCTATCGCTACA 1960

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Db 2381 TTXACCTTCTGCGATGATGAGGCACACT 2410

RESULT 6

AB022091
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DEFINITION Citrus unshiu CitsUSA mRNA for sucrose synthase, complete cds.
ACCESSION AB022091
VERSION AB022091.1 GI:6682840
KEYWORDS sucrose synthase.
SOURCE Citrus unshiu
ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE 1
AUTHORS Komatsu, A., Moriguchi, T., Koyama, K., Omura, M. and Akihama, T.
TITLE Analysis of sucrose synthase genes in citrus suggests different
roles and phylogenetic relationships
J. Exp. Bot. 53 (366), 61-71 (2002)
MEDLINE 21606208
PUBMED 11741042
REFERENCE 2 (bases 1 to 2765)
AUTHORS Komatsu, A.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1998) Akira Komatsu, National Institute of Crop
Science; 2-1-18, Tsukuba Science City, Ibaraki 305-8518, Japan
(E-mail: akomatsu@affrc.go.jp, Tel: 81-298-38-8949,
Fax: 81-298-38-8949)
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ORIGIN

Query Match 49.1%; Score 1353.4; DB 8; Length 2765;
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Matches 1769; Conservative 0; Mismatches 666; Indels 6; Gaps 1;

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 ACCESSION AJ001071
 VERSION AJ001071.1 GI:2570066
 KEYWORDS sucrose synthase.
 SOURCE Pisum sativum (pea)
 ORGANISM Pisum sativum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
 Pisum.
 REFERENCE 1
 AUTHORS Buchner, P., Poret, M. and Rochat, C.
 TITLE Cloning and Characterization of a cDNA (Accession No. AJ001071).
 JOURNAL Encoding a Second Sucrose Synthase Gene in Pea (Pisum sativum L.)
 REFERENCE 2
 JOURNAL Plant Physiol. 117, 719-719 (1998)
 AUTHORS Buchner, P.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-1997) Buchner P., Metabolisme, INRA-Versailles,
 Route de St. Cyr, Versailles-cedex, 78026, FRANCE
 REMARK Revised by [3]
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 JOURNAL Buchner, P.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-1997) Buchner P., Metabolisme, INRA-Versailles,

Route de St. Cyr, Versailles-cedex, 78026, FRANCE
On Oct 28, 1997 this sequence version replaced gi:2326794.

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Location/Qualifiers

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CDS

3'UTR
polya_signal
ORIGIN

Query Match 49.0%; Score 1352.2; DB 8; Length 2848;
Best Local Similarity 72.9%; Pred. No. 9.3e-217;
Matches 1757; Conservative 0; Mismatches 648; Indels 6; Gaps 1;
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1683 CATTTGGCATCTGATGACCGGTCAAGCCCATCTCTCTCCATGCGACGATCGACAG 1742
Db |||||||
1801 CATTTGGTCTACTGACACCGGTCAAGCCCTATTAATTTTCCATGCGAAGCGCTAGACAG 1860
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1981 AATTGAAGATCGAAGAGATGATGATCTCATGAAGCAATACAACTTTGAATGGCGAGTT 2040
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Db |||||||
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Db |||||||
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Db |||||||
2521 TCCATAGCAA 2531

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RESULT 8
LOCUS AB045710
DEFINITION Pyrus pyrifolia PypSUS1 mRNA for sucrose synthase 1, complete cds.
ACCESSION AB045710
VERSION AB045710.1 GI:12032280
KEYWORDS Pyrus pyrifolia (sand pear)
SOURCE Pyrus pyrifolia
ORGANISM Pyrus pyrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
REFERENCE 1

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AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
FEATURES
source

Tanase, K., Shiratake, K., Mori, H. and Yamaki, S.
Changes in the phosphorylation state of sucrose synthase during
development of Japanese pear fruit
Physiol. Plantarum 114 (1), 21-26 (2002)
11982930
2 (bases 1 to 2787)
Tanase, K., Yamaki, S. and Mori, H.
Direct Submission
Submitted (30-JUL-2000) Koji Tanase, Nagoya University, Graduate
School of Bioagricultural Sciences; Chikusa, Nagoya, Aichi
464-8601, Japan (E-mail: i000043r@box.media.nagoya-u.ac.jp,
Tel: 81-52-789-4028, Fax: 81-52-789-4025)
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gene
CDS
ORIGIN

Query Match 47.7%; Score 1316; DB 8; Length 2787;
Best Local Similarity 71.5%; Pred. No. 1.1e-210;
Matches 1746; Conservative 0; Mismatches 690; Indels 6; Gaps 1;

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Db 165 CCGTAAGCAACTGTTGCCCTCTCTCAGTACTGATCAGGGGAAGAATACTGCA 224
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Db 225 GCGGACACCATGATGATCAGCTCGACATTTGTCATCGGCGAGATGAAGCAACACGCA 284
Qy 183 GCTCGCGGAGGACCTTCTCTCGACGCTCTCGGTCGCGGACGAGGAGTCTGCTGCC 242
Db 285 GCTCAAAAATGGACCTTTCAGCGAAGTCTCAATCCGACACAGGAACATTTCTGCGC 344
Qy 243 GCGGTCGTCGCGCATCGGTCGCGCGCGCGCGGAGTTGGGAGTACGACGTCGCGTCAA 302
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Qy 303 CGTTACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCGGCTTCAAGGAGA 362
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465	Db	ACTTGTAGATGGGAGTCTAGTGCACAAATATGATCTTGAGCTCGACATTGAGCCATTAA	524
423	QY	TGCTCAGTCCAGCGCCCAATCGGTCACTCATCTATTGSAAGAGGTGTGAGTTCCTCAA	482
525	Db	TGCTGCTTTTCTCGTCCACCCGATCTTATCCATTGGAATGGTGTCAAATTTCTCAA	584
483	QY	CCGACACTTGTCCCTCAATCATGTGTTCCGCAACAGCGGATGCTTGAGAGCCCTGTGGAATT	542
585	Db	CCGCCACTTTCTCAATATGTTCCGTAAACAGAGATCGTTGATCCATTACTTGATTT	644
543	QY	CTCCGTGGCCACCGGCACAGGGGCGATGTATGATGCTTTAATGATAGATACAAAGCTT	602
645	Db	CTTAGAGCACACAAATATAAAGGCCATCCATTGATGTAATGATCCGATACAGAGCGT	704
603	QY	GGGAGGCTTCAGTCTGTGTGACCAAGCTGAGGACACTTGTTCAAGCTCCCTGCTGA	662
705	Db	ATCCAGCTTCAGTCAGCTTTAGCTAAGGCTGAGGATCATCTTTCCAAAGCTTCAACCCGA	764
663	QY	CACACCATACTCAAAATTTGCTTATAAATTTCAAGAGTGGGGCTGCAGAAAGGTTGGGG	722
765	Db	GACACCTACTCTGAGTTTGAATAATTATTTCAAGGAATGGGTTTTCAGCGAGTTGGGG	824
723	QY	TGATACAGCAGGACATGTTTGGAAATGATCCATCTCTCTTACAGATCATCATCAGCGCC	782
825	Db	CGATACTGCAGTACACGTAATTGGAGATGATGTCATCTCTCTAGATATCCTTCAGGCTCC	884
783	QY	AGACCATCTACCTAGAGAAATCTTGGGGAGATCCCATGATGTTTTAACTGTTGT	842
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843	QY	GGTATCCCTCATGGATACTTTGGTCAAGCTAATGTATTAGGCTTGCACACACAGGAGG	902
945	Db	TTTGTCTCCATGGATACTTTGGACAGCAATGTTTAGGCTTACCCGACACTGGTGG	1004
903	QY	ACAGATGCTCTATACTGGACCAAGTCCGTGCATAGAAATATGAGATGGTCTTCOGTTT	962
1005	Db	CCAGATTGCTATATCTATGACCAAGTCCGCGCCCTCGAAAAAGAAATGCTCGAAAGAAT	1064
963	QY	AAAGAAACAGGCTGTATGTTTTCCCAAGATTTCTATTGTTTACTCGGCTGATACCGA	1022
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1083	QY	CATTTAAGAGTTCCCTTCAGAAATGAATGGGATATCTTAAGAAATGGATATCAAGATT	1142
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1323	QY	TAGATCCAGATTCAGACATATTTTGGAGAAATTTGATGAGAAGTACCAATTTCTCTTG	1382
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1485	Db	TCAGTTTCAOGGCTGATCTTATTGCCATGAATAAGCAGATTTTCATATCACCAGCACATA	1544
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Q5	1503	TCTGCCCTGTCGTACCGAGTGTCCATGGATCGATGCTCTCGATCCAAAGTTCAAATAT	1562
D5	1605	TCTTCTCGGCAGTACCGAGTGGTTCATGGAAATATATGCTTTTGATCCAAAGTTCAAATAT	1664
Q5	1563	AGTCTCTCTCGAGCTGACATGTCATATATCTTTCCACATACCGAGAAGCCCAAGCGACT	1622
D5	1665	CGTGTCTCCCGGAGCAGATAGACCAATTAATTTCCCTACTCTGAAAGCAAAAGAGACT	1724
Q5	1623	CACCTCTCTCATGCTTCATCGAAATTTGATTTATGACCCGAGCAAAACGATGAACA	1682
D5	1725	TACGAGCTTCATGGTTCCTTAGAAGATGCTATATAATCTCTGACCGAGATGATGTTCA	1784
Q5	1683	CATTGGGCATCTGGATGACCGGTCAAAGGCCATCTCTTCTCCATGSCGAAGATCCGACAG	1742
D5	1785	TATTGGCACACTAAGCGATCGATCAAAGCCCAATAATTCTCAATGCGAAGGCTCGACCA	1844
Q5	1743	GGTGAAGACATATAACAGGCTGTGCGAAGCTTTTGCTAAGTGGCTTAAGCTGAGGAGCT	1802
D5	1845	GGTGA AAAATATGACTGGGTGGTTCGAGTCTATGCTAAATGTTCCAAATCGAGGATCT	1904
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D5	1965	AATTGCAGAGATTGAGAAGATGATTAATCTTATGATTGAGTATCAAAATTAGATGGTCAATT	2024
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Q5	1983	TGATACCCATGFGTCTTTGGTACAGCGGCGCTTGTAAGAAGCGTTTCGCTCACCGTCTGT	2042
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Q5	2043	TGAGGCCATGACCTGTGGGCTTCTACTTTGCGAGCTCCATGAGAGTTCGAGCTGAGAT	2102
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Q5	2283	GATGACATCTGGCGGGGTCTACGGTTTTCGGAAGTACGTGTGGAAGCTCGAGAGGCTGGA	2342
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D5	2445	GACCGACGTTATCTGGAGATGTTCTACATTCGTAAGTTTCGTGATTTGGCAAAATCTGT	2504
Q5	2403	GCGCTTGCAAATGACCAACCGCAGTAGCTTCGCGAACTGGG	2444
D5	2505	TCTCTGAAGCCATTGATGATGCACATTAAGTTCAACTGCTGAG	2546

RESULT 9	AY205302
AY205302	Solanum
LOCUS	AY205302
DEFINITION	
ACCESSION	

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VERSION      AY205302.1  GI:29289942
KEYWORDS
SOURCE       Solanum tuberosum (potato)
ORGANISM     Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE    1 (bases 1 to 2679)
AUTHORS      Loureiro,M., Kopka,J., Mueller-Roeber,B. and Trethewey,R.
TITLE        Characterization of effects of specific reduction in gene
              expression of two sucrose synthase genes in transgenic potato
              plants
              Unpublished
              2 (bases 1 to 2679)
              Kopka,J., Loureiro,M., Mueller-Roeber,B. and Trethewey,R.
              Direct Submission
              Submitted (20-DEC-2002) Plant Biology, Federal University of
              Vicosa, Av PH Rolfs S/N, Vicosa, MG 36570-000, Brazil
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              ORIGIN
              Query Match      45.9%; Score 1264.8; DB 8; Length 2679;
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              DB      |||
              QY      82  TCTGCTCACCGTAATCAGCTAGTGGCTCTCTATCGAGATATGTGGCGAGGGGAGGGG 141
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              QY      121  ATCTCTGACGCGCACACATCTCTGACGCGCTC-----GACAGGTCCAGGGCTCGGG 174
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              QY      142  ATATTTGCAACCTCATCACTTAATTTGATGAGTTCAATAGTGTCTGATGATGACACTGCT 201
              DB      |||
              QY      175  GTCCGCGCGCTCGCGGAGGACCTTCTCTGACGCTCTCGCTCCGCGGAGGAGGGATC 234
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              QY      202  TGTGAAGACTCAAGAGAGCCCTTTTGTGAATCTTGAATCTACTCAGGAAGCCAT 261
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              QY      235  GTGCTGCCCGCTTCTGTGGCCATTCGGGTGCGCGCCCGCGCGGAGTTTGGGAGTAGCTC 294
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DB      382  AAAGAAGAAGCTTGTGAGTGGAGAGGATAAATAATCTCTTTGTGCTTGAGCTGGAATTGA 441
QY      415  CCGTTCATGCTCAGTCCCAAGCGCCCAATCGGTGATCATCTTTTGGAAAACGTTGAG 474
DB      442  CCATTTAATGATCAGTTCTCGCTGCTCATCACGCTCTTTCATCTTTGGAATGAGTCCAA 501
QY      475  TTCTCAACGACACTTGTCTCAATCATGTTCCGCAACAGGAGATTGTTGAGGCCCCCTG 534
DB      502  TTCTCAATCGTCAATTTGTCTCAATAATGTTTCGACCAAGAAATCTCTCGACCCGTTA 561
QY      535  TTGAATTTCTTCCGTGCGCACCGGCAACAAGGGGCAATGTTATGCTTTAATGATAGAATA 594
DB      562  CTTGAATTTCTTAGAGGACCAATCATAAAGGGAATGTCTTGATGTTTGAATGAAGCTATA 621
QY      595  CAAAGCTTTGGGAGGCTTCAGTCTGTGCTGACCAAAAGCTGAGGAGCACTTCTCAAAGCTC 654
DB      622  CAGGGAATCTCCAGGCTGGAGTGTCTCTTAATAAGCAGATGATTAATCTCTCAAGCTA 681
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QY      775  CAGGCGCCAGACCCATCTACCTTAGAGAAATTTCTGGGAGGATCCCATCATATTTTAAC 834
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DB      862  GTTGTGATATATCTCTCATGATATCTTGGTCAAGCAAAATGCTTGGGTTTGGCGGAC 921
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QY      955  CTCCTGTTTAAAGAAAACAAGGCTTGAATTTTCCCAAGATTTCTATTGTTTACTCGGCTG 1014
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DB      1042  ATACCTGATGCTAAAGGAACCAAGTGCACACGCGTTGGAGAGAAATTAGTGGAACTGAA 1101
QY      1075  CATACTTACATATTAAGGTTCCCTTCAGAAATGAAATCGGATACCTTAAGAAATGATA 1134
DB      1102  TACTCACATATTTAGTGTCCTTTTAGACAGAAAATGAAATCCTTCTATAATGATA 1161
QY      1135  TCAAGATTTGATGTGGCCATATCTGGAACATTTTCTGAGGATGCTGCTGTGAATTT 1194
DB      1162  TCTAGGTTTGAATGATGCTTACCTGAGAGAGTTTACTGAGAACGTGGCAGGTGAATG 1221
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DB      1282  GTTGCTTCCCTGTAGCATATAAATGGGCGTCAACAGTGTACCATTTGCTCATGCTTTG 1341
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 QY 1495 GCCTTTACTCTGCTCTGTCTGTACCGAGTTCCTCATGGATCGATCTTCGATCCAAAG 1554
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 Db 1642 AGAGACTGACATCTTGCATCTCTGATTTGAGAGTTGTTATTTGATCTGAGCAGAT 1701
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 QY 1855 AGGAAAGATCGCGGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1914
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 Db 1942 GGTCAATTCAGATGAGATATACGCCAAATTAACCGGGCAGTAAATGGTGAAGCTCTATCGC 2001
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RESULT 10
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 LOCUS

CPL:32000 2648 bp mRNA linear PLN 25-AUG-1999

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Craterostigma plantagineum mRNA sucrose synthase 2.

AU132000

AU132000.1 GI:4468152

ss2 gene; sucrose synthase.

Craterostigma plantagineum

Craterostigma plantagineum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Lamiales; Craterostigma.

REFERENCE AUTHORS

Kleines M., Elster, R.C., Rodrigo, M.J., Blervacq, A.S., Salamini, F. and Bartels, D.

Isolation and expression analysis of two stress-responsive sucrose-synthase genes from the resurrection plant *Craterostigma plantagineum* (Hochst.)

Planta 209 (1), 13-24 (1999)

99396657

10467027

2 (bases 1 to 2648)

Kleines, M.

Direct Submission

Submitted (25-FEB-1999) Kleines M., Abteilung fuer

Pflanzenzuechtung und Ertragsphysiologie, Max-Planck Institut fuer

Zuechtungsforschung, Carl von Linne Weg 10, D-50829 Koeln, GERMANY

Location/Qualifiers

FEATURES

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DEFINITION Sequence 2415 from Patent WO0216655.
ACCESSION AX507720
VERSION AX507720.1 GI:23388957
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
1 Harper, J.F., Krens, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 2415 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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Matches 1693; Conservative 0; Mismatches 712; Indels 6; Gaps 1;
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 VERSION AY142511.1
 KEYWORDS Arabidopsis thaliana (thale cress), FLI CDNA.
 SOURCE

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids;

REFERENCE
AUTHORS

1 (bases 1 to 2506)
 Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Heuan,V.W.,
 Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wallender,E.K., Wong,C.,
 Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
 Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J.,
 Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
 Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE
JOURNAL
REFERENCE
AUTHORS

Arabidopsis Open Reading Frame (ORF) Clones
 Unpublished

2 (bases 1 to 2506)

Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
 Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K.,
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 Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
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 Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE
JOURNAL

Direct Submission
 Submitted (16-AUG-2002) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA

COMMENT

The RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
 sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yamada,K.,
 Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Heuan,V.W., Lee,J.M.,
 Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C.,
 Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
 Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T.,
 Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
 to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
 /PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
 genome submitted to GenBank.

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 JOURNAL
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 Submitted (11-Sep-2001) Salk Institute Genomic Analysis Laboratory
 (SIGAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
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 Arabidopsis thaliana (thale cress)
 JOURNAL
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 Submitted (11-Sep-2001) Salk Institute Genomic Analysis Laboratory
 (SIGAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 COMMENT
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN

Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGE (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H.,
 Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L.,
 Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G.,
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 Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
 Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
 contributed equally to this work as PIs.

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RESULT 14
AY051001
LOCUS

AY051001 2904 bp mRNA linear PLN 18-SBP-2002

DEFINITION Arabidopsis thaliana putative sucrose synthetase (At4g02280) mRNA, complete cds.

ACCESSION AY051001

VERSION AY051001.1

KEYWORDS GI:15293134

SOURCE FLI CMAA

ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE 1. (bases 1 to 2904)

AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Gierg,P.X., Lee,J.M., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shimn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Arabidopsis Full Length cDNA Clones

JOURNAL Unpublished

REFERENCE 2. (bases 1 to 2904)

AUTHORS Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Gierg,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shimn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Direct Submission

JOURNAL Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shimn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

source

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1. .214

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215. .264

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5'UTR

CDS

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2645. .2904

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3'UTR

ORIGIN

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LOCUS 2706 bp mRNA linear PLN 25-AUG-1999
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 asterids; lamiales; Lamiales; Crataegales; Crataegales; Crataegales;
 Craterostigma.

REFERENCE AUTHORS

Kleines M., Elster, R.C., Rodrigo, M.J., Biervacq, A.S., Salamini, F.
 and Bartels, D.
 Isolation and expression analysis of two stress-responsive
 sucrose-synthase genes from the resurrection plant Craterostigma
 plantagineum (Hochst.)

JOURNAL Planta 209 (1), 13-24 (1999)

MEDLINE 99396657

PUBMED 10467027

REFERENCE 2 (bases 1 to 2706)

AUTHORS Kleines, M.

TITLE Direct Submission

SUBMITTED (25-FEB-1999) Kleines M., Abteilung fuer

Pflanzenzuzuechtung und Ertragsphysiologie, Max-Planck Institut fuer

Zuechtungsforschung, Carl von Linne Weg 10, D-50829 Koeln, GERMANY

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QY 1766 TCSAGCTTTTTCCTAAGTGGCTAAGCTGAGGAGCTGGTAAACCTTGTGCTGTTGCCG 1825
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1880 TTGAATGTACGCCCAAGAACAAAAGCTGAGAGACTCACCAACCTCGTGGTGGTTCGCCG 1939
QY 1826 GGTACATGATGTCAACAAATCCAGAGACAGGAGAGATCGCGAGATAGAGAGATGC 1885
Db |||||
1940 GTTACAGGAGCTGAGAGATCGAGCGACAGAGAGAGAGAGAGAGATAGAGAGATGC 1999
QY 1886 ATGAATCATCAAGACCCACAACTTGTTCGGGCAATTCGGTGGATCTCTGCCACAGCAA 1945
Db |||||
2000 ACAACCTCATCGACAGTACGACTTGAACGGAAGCTTGGGTGGATATCTGCCAGAGCA 2059
QY 1946 ACAGGCCCCGTAAAGGCGAGCTCTATCGCTACATCGCTGATACCCATGGTGTTCGTAC 2005
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2060 ACAAGCTCGCAAGCGGAGCTTACCGTTTATCTTATCTGATAGCTGACAAGAGGGGGATA 2119
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QY 2066 CTACTTTCGCAAGCTTCATCGAGTCCAGGTCCAGCTGAGATCATAGAGCATGGCGTCTCGGCT 2125
Db |||||
2180 CTGGGTTGCAACTCTCCACGGTGGGCCCCACGAGATCATCGAAGACGGTGTGCGGAT 2239
QY 2126 TCCACATTGACCCGTACCCACCGACAGAGCTGTTATCTGATGSCCGACTTCTTCGACC 2185
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2240 TTCAATAGATCCATACCATGCCGAAAGCTGCGACTCGCATGCTGATTTTTCGCCA 2299
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QY 2366 TCTACATCTGAAGTTCGCGAGCTGGCGAGACCGGTGCCCTTGCATTTGA 2417
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Search completed: May 25, 2004, 19:58:58
Job time : 7069.61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 15:35:16 ; Search time 133.484 seconds
(without alignments)
11462.031 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

Sequence: 1 atgtctgcccgaagctgaa.....aaaaaaaaaaagggcgccgc 2757

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:**

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:**

2: /cgn2_6/ptodata/2/ina/5B COMB.seq:**

3: /cgn2_6/ptodata/2/ina/6A COMB.seq:**

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5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:**

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177.8	42.7	2563	2	US-08-553-436A-7
2	1131	41.0	3103	4	US-09-598-401C-57
3	482.8	17.5	2700	4	US-08-684-005-1
4	229.2	8.3	265	4	US-09-313-294A-1862
5	155	5.6	6386	2	US-08-483-376-1
6	142	5.2	532	4	US-09-598-401C-56
7	117.2	4.3	272	4	US-09-313-294A-1221
8	111.8	4.1	271	4	US-09-313-294A-1826
9	89.8	3.3	3509	1	US-08-175-471-6
10	89.8	3.3	3509	2	US-08-175-471-6
11	89.8	3.3	3509	3	US-09-078-862-2
12	89.8	3.3	3509	3	US-09-051-341-6
13	89.8	3.3	3509	4	US-09-866-153-12
14	89.8	3.3	3509	4	US-09-693-467A-12
15	80.4	2.9	3509	2	US-08-429-054A-12
16	63.8	2.3	3524	4	US-09-697-367-15
17	61.6	2.2	3635	2	US-08-553-436A-5
18	58.2	2.1	417	4	US-09-252-991A-14336
19	58.2	2.1	1449	4	US-09-252-991A-14399
20	58.2	2.1	1824	4	US-09-252-991A-14307
21	58.2	2.1	2236	4	US-09-697-367-1
22	58	2.1	210	3	US-09-125-984-1
23	57.6	2.1	1926	4	US-09-249-585A-4
24	57.6	2.1	1931	2	US-09-130-114-2
25	56	2.0	15872	3	US-09-105-537-1
26	56	2.0	15872	4	US-09-091-609-1
27	56	2.0	15872	4	US-09-091-609-3

28	55.8	2.0	1191	4	US-09-252-991A-8126	Sequence 8126, Ap
29	55.8	2.0	1560	4	US-09-252-991A-8114	Sequence 8114, Ap
30	55.8	2.0	1709	4	US-09-594-193-12	Sequence 12, Appl
31	55.8	2.0	2571	4	US-09-252-991A-8190	Sequence 8190, Ap
32	55.6	2.0	1908	1	US-08-173-508-1	Sequence 1, Appli
33	55.6	2.0	1908	2	US-08-265-310-1	Sequence 1, Appli
34	55.6	2.0	1908	3	US-08-951-742-1	Sequence 1, Appli
35	53.8	2.0	2098	1	US-08-153-848-41	Sequence 41, Appl
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37	53.8	2.0	2098	4	US-09-088-337B-41	Sequence 41, Appl
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40	52.6	1.9	1314	4	US-09-252-991A-1265	Sequence 1265, Ap
41	52.6	1.9	1482	4	US-09-252-991A-1338	Sequence 1338, Ap
42	52.6	1.9	1671	4	US-09-252-991A-1222	Sequence 1222, Ap
43	52.4	1.9	12001	1	US-08-458-568A-11	Sequence 11, Appl
44	51.6	1.9	1693	3	US-09-320-878-23	Sequence 23, Appl
45	51.6	1.9	1693	4	US-09-141-908-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-08-553-436A-7

; Sequence 7, Application US/08553436A

; Patent No. 5866790

; GENERAL INFORMATION:

; APPLICANT: HESSE, Holger

; APPLICANT: MULLER-ROBER, Bernd

; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

; TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE

; TITLE OF INVENTION: CONCENTRATION

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10036-8403

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/553,436A

; FILING DATE: 17-NOV-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP94/01671

; FILING DATE: 20-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 4317596.1

; FILING DATE: 24-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Meilman, Edward

; REGISTRATION NUMBER: 24,735

; REFERENCE/DOCKET NUMBER: P/951-117

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 382-0700

; TELEFAX: (212) 382-0888

; TELEX: 236925

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2563 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Beta vulgaris

INDIVIDUAL ISOLATE: Saccharosynthesinase
IMMEDIATE SOURCE:
LIBRARY: phage lamda zap
FEATURE:
NAME/KEY: CDS
LOCATION: 3..2303
US-08-553-436A-7

Query Match 42.7%; Score 1177.8; DB 2; Length 2563;
Best Local Similarity 70.9%; Pred. No. 6e-290;
Matches 1592; Conservative 0; Mismatches 647; Indels 6; Gaps 2;

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Db
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2101 ATCATAGAG 2160
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1941 ATTATAGAG 2000
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Db 2238 GTTCGCTGGCAACAGATGAAGAGC 2262

RESULT 2
US-09-598-401C-57
; Sequence 57, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c2
; CURRENT APPLICATION NUMBER: US/09/598,401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 3103
; TYPE: DNA
; ORGANISM: Eucalyptus grandis

US-09-598-401C-57
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Best Local Similarity 66.9%; Pred. No. 5.5e-278;
Matches 1624; Conservative 0; Mismatches 800; Indels 3; Gaps 1;
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Qy 61 CACGCGACCCCAACGAGCTCGTCCGCTCTCTCCAGTACGTGAACAAAGGGAAGGSC 120
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Qy 601 TTGGGGAGGCTTCAGTCTGTGCTGCTGACCAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCT 660
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Qy 661 GACACACCATACTCAAAATTTGCTTATAAATTTCAAGAGTGGGGCTCGAGAAAGGTTGG 720
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Qy 721 GGTGATACAGCAGGACATGTTTGGAAATGATCCATCTCTCTTAGACATCATTCAGGCG 780
Db 1167 GGTGACAGGCTGAGCGCTCCTCGAGATGATCCAGCTCTCTGTTGGATCTCTCTTGAAGCT 1226
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Db 1227 CCGGACCCGTGCACTCTCGAAGATTTCTTGGATAGGGTTCCCATGCTTCTTCAAGCTG 1286
Qy 841 GTGGTATCCCTCATGAGTACTTTGCTCAAGCTTAATGATTTAGGCTTGCACACACAGGA 900
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Db 1407 ATTAAGCAACAGGACTGATATCTCTCGATTTCTCATTTACTCTCGGCTTCTTCCA 1466
Qy 1021 GATCAAAAGGAACATCATGCAATCAGCGGCTTGAAGAAATTAGTGAACACACAGATACT 1080
Db 1467 GACGCGGTTGGAACCACTGTCGCGCAGCGCTTGAAGAAATTTTGGGACCGGACTACTCC 1526
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Qy 1141 TTTGATGTGCGCCATATCTGGAACATTTCTGAGGATGCTGCTGTTGAATTCGCTGCT 1200
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Qy 1201 GAATTAAGGTACTTCCAGACTTCTAATTTGAAACTACAGTGAAGTGAAGTGAAGTGAAG 1260
Db 1647 GAGTTGAGGCGAAGCTGATCTGATCATCGAAGTACAGTGAAGTGAAGTGAAGTGAAGTGA 1706
Qy 1261 TCATTTGCTTCTTACAGATGGGAATTAACCAAGTGAACATTTGCTCATGCTCTGGAAG 1320
Db 1707 TCTTTGTTAGCATAAATTAGGTGTTTACAGATGATACATAGCCCATGCTTCCGAGAG 1766
Qy 1321 ACTAAGTATCCAGATTCAGACATATTTTGGAGAGATTTGATGAGAGTACCATTTCTCC 1380
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Qy 1381 TGCCAGTTCAGTCTGATATAATTTGCTATGAACATGCTGATTTTATCATCACCAGCACA 1440
Db 1827 TGCCAGTTCAGTCTGATCTCTGTCGCCATGAAACACCGACTTCTATTTATCACCAGACC 1886

QY 852 TCATGGATACCTTTGGTCAAGCTAATGTATTAGGCTTTGCCAGACACAGGAGGACAGATCGT 911
Db 1084 CCACGGTTGGTTCCGACAGAGGGGGTTTAAAGTCGTCAAGTACTGGTGGTCAAGTAGT 1143
QY 912 CTATATATCTGACGCAAGTCCGTGCACTAGAAATAGAGATG-----GTTCCTCGGTTT 962
Db 1144 GTAGCTCTTCCACCAAGCTAAGAAATTTAGAAAAGCACTGCAAGAAGATGCCATATTGC 1203
QY 963 AAAGAAACAAGGGCTGTATGTTTCCCAAGATTTCTCATGTTACTCGGCTGATACCGAGA 1022
Db 1204 AGGTTTAGAGGATTTGAACGCTCCAGCCCAAGGTAAATTAATCTCAACCGCTCTGATTCCTAA 1263
QY 1023 TSCAAAAGGAACATCATCAATCAGCGCTTGAGAGAAATAGTGAACACACAGCATACTTA 1082
Db 1264 TAGTGAGGAAACGCTTTGTATACCAAGGTTAGAAAAGTCTACGGTACAGAGAACGCGCTG 1323
QY 1083 CATATTAGGAGTTCCTTTCAGAAATGAAATGGGATCTTA---AGAAATGGATATCAAG 1139
Db 1324 GATTTTGGGTTAGCTCTCGCGGAGTTTAAACCCCAAGATGACGCAAGTCTGGAATTTCTG 1383
QY 1140 ATTTGATGTGGCCATCTCTGGAACATTTGCTGAGGATGCTGCTGTGAAATTTGCTGC 1199
Db 1384 ATTCGAGTTTGGGCTTATCTAGAAACCTTTGCCAATTCAGTCTCAGAAAAGAAATTTGTGCG 1443
QY 1200 TGAATTACAAGGTACTCCAGACTTCATAATTTGGAACACTACAGTGTGATGAAATCTGTGCG 1259
Db 1444 AGAATTCMAAGTAGACCAAGCTTAACTGCTGGGTAAATTAATCTAGCGGAACTTAGTTGC 1503
QY 1260 GTCAATTCGACTTACAAGATGGGAATTTACCCAGTGCACAAATGCTCATGCTCGGAAAA 1319
Db 1504 TTTTCTGTGACGCGAGGATGAAAGTTACCCATGCAACATGCTCATGCTTTAGAAAA 1563
QY 1320 GACTAAGTATCCAGATTCAGACATATTTTGAAGAATTTGATGAGAAGTACCATTTCTC 1379
Db 1564 ATCCAAATCTGTTTGTAGTAACTCTACTGCGCAAGATTTGGAAGAAAATATCATTTCTC 1623
QY 1380 CTGCCAGTTCACTGCTGATATAATTTGCTATGAACAATGCTCATTTTATCATCACCGAC 1439
Db 1624 TTTACAAATTCACGCTGATTTAATAGTATGAATGCTGCTCACTGCTCATCACGAGC 1683
QY 1440 ATACCAAGAAATTCCTGGAGCAAAAATATCTGTTGACAGTATCAGAGTACATCTGCTT 1499
Db 1684 CTATCAAGAAATTTGTGGCACACCCAGACAGTATAGGCGAGTATCAGTCTTACAATGCTT 1743
QY 1500 TACTCTGCTGCTGTGACGAGTTGCTCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1559
Db 1744 TACATGCGGAACTGATCATGTTGGTCAACGCGCAATTTAATTTAGCCCCCAATTTAA 1803
QY 1560 TATAGTCTCTCTGGAGCTGACATGTCCATATATCTTTCCACATACCGAGAGGCCAAGCG 1619
Db 1804 CGTTGTACCGCTGTGTGAATGAABATTCCTACTTTCCCTACACAACTCAAAACAG 1863
QY 1620 ACTCACTCTCTTCATGTTTCAATCGAAATTTGATTTATGACCCGAGCAAAACAGTGA 1679
Db 1864 ATAGAAAGCGATCGGATCGCTTAGAGGAATGCTGTTTACCCCTAGAAGATTTAGCCA 1923
QY 1680 ACACATGGCCATCTGATGACCGGTCAAGAGCCATCTCTTCTCCATGCGAAGCTGGA 1739
Db 1924 ATCTTTCGGCAAACTGACACCCCAATAAGGCTCTTAATTTTCTCAATGGCGGACTTGA 1983
QY 1740 CAGGGTGAAGAAATACAGGGCTGTGCGAGCTTTTGTGCTAAGTGGCGCTAAGCTGAGGA 1799
Db 1984 CCGAATTAATAAATCTCACAGTTTGGCAGAAATGCTTTGGTCAAGTCAAGAAATTCAGAA 2043
QY 1800 GCTGGTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1859
Db 2044 ACCTTGCAACTTAATTTAGTTGAGTAAAGTGGGTATCGAAGATCAGAAATACAGTA 2103
QY 1860 AGAGATCGCGGATAGAGATGATGAATCTCATGCAAGCCCACTGCTGCTGCTGCTGCTG 1919
Db 2104 AGAAAAGACGAAATCTCAAACTTTACCGGATTTATTGAGCAATACTCAACCTGCTGCA 2163

QY 1920 GTTCGCTGGATCTCTGCCAGACAAACAGGGCCCCCTAAACGGGAGCTCTATCGCTACAT 1979
Db 2164 AATTGCTGGTTAGGTGTGCGCTTATCCAAAAATGACTCCGGTGAATTTATCGCGTCAT 2223
QY 1980 CGCTGATACCCATGCTGCTTCTGTAAGCCGCTGCTGATGAGCGCTTCGGTCTCAAGCT 2039
Db 2224 TTGCGATCGCAAGGCAATTTTGTACAGCCAGCAATTTTGAAGCCCTTTGGGGTTGCAAT 2283
QY 2040 CTTGAGGCAATGACCTCTGCGGCTTCTCTACTTTTCGCAAGCTCCATGGAGGTCAGCTGA 2099
Db 2284 CTTGAGTCAATGATTTCCGGATTGCAACATTTGCTACCCCAATTTGGGGGCCATTGGA 2343
QY 2100 GATCATAGAGATGCGGCTCTCGGCTTCTCAATTTGACCGCTACACCCTCCGAAACAGGCTGT 2159
Db 2344 GATTATTCAAGGATAAGATTAATGCGCTTCTACATTAACCTTACTCATCTAGAGAAACAGC 2403
QY 2160 TAACTGATGCGCGACTTCTTCGACGGTGCAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2219
Db 2404 CACAAAATTTCTGATTTCTGTCACCAATGCGAACAATCTTAATTTTGGAAACATAAT 2463
QY 2220 ATCTGAGACGGCTGCGAGCGCATATACGAGAAGTACACATGGAAGATATATCTCAGAGAG 2279
Db 2464 TTCCGAGAAAGCAATTCAGAGATATATAGTACATACACCTTGGAAATATACACAACTAA 2523
QY 2280 GTTGTATGACCTGCGCGGCTCTAGGCTTCTGGAAGTACGCTGCGAAGCTCGAGAGGCT 2339
Db 2524 GCTGTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2583
QY 2340 GGAGACGAGGCGCTACCTTTGAG 2361
Db 2584 AGATTTATTACGCTACCTTTGAG 2605

RESULT 4

US-09-313-294A-1862
; Sequence 1862, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1862
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551647H1
US-09-313-294A-1862

Query Match 8.3%; Score 229.2; DB 4; Length 265;
Best Local Similarity 95.9%; Pred. No. 7.1e-49;
Matches 257; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 474 GTTCCTCAACCGACACTTGTCTCAATCATGTTCCGCAACAGGATGCTTTGGAGCCCT 533
Db 1 GTTCCTCAACCGACACTTGTCTCAATCATGTTCCGCAACAGGATGCTTTGGAGCCCT 60
QY 534 GTTGGATTTCTCGTGGCCACCGGCAAGGGGCAATGATGCTTAATGATGAAT 593
Db 61 GTTGGATTTCTCGTGGCCACCGGCAAGGGGCAATGATGCTTAATGATGAAT 119
QY 594 ACAAGCTGGGAGGCTTCAAGTCTGTGCTGACCAAGCTGAGAGCACTTGTCAAAGCT 653
Db 120 ACAAGCTGGGAGGCTTCAAGTCTGTGCTGACCAAGCTGAGAGCACTTGTCAAAGCT 179
QY 654 CCTGCTGACACACCTACTCAAAATTTGCTTTAAATTTCAAGAGTGGGCGCTTGAGAA 713

Db 180 CCCTGCTGACACATCACTACCAATTTGCTATTAATTTTCAGAGTGGGGC--TGGAGA 237

Qy 714 AGGTGGGGTGATACAGCAGGACATGTT 741

Db 238 AAGTGGGGTGATACAGCAGGACATGTT 265

RESULT 5

US-08-483-376-1
; Sequence 1, Application US/08483376
; Patent No. 595330
; GENERAL INFORMATION:
; APPLICANT: Vasil, Vimla
; APPLICANT: Clancy, Maureen A.
; APPLICANT: Ferl, Robert J.
; APPLICANT: Vasil, Indra K.
; APPLICANT: Hannah, L. C.
; TITLE OF INVENTION: No. 595330a1 Means for Enhancing Gene
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,540
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,115
; FILING DATE: 04-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/830,956
; FILING DATE: 05-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/353,854
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Jocna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 10-94B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: ENA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: Black Sweet
; FEATURE:
; NAME/KEY: exon
; LOCATION: 131..182
; FEATURE:
; NAME/KEY: exon

; LOCATION: 1211..1324
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1828..1948
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2041..2187
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2269..2460
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2605..2728
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2822..3038
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3256..3351
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3447..3620
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3702..3818
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3912..4078
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4158..4381
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4517..4835
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4768..5212
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5372..5510
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5636..5917
; US-08-483-376-1

Query Match 5.6%; Score 155; DB 2; length 6386;
Best Local Similarity 70.5%; Pred. No. 3e-29;
Matches 222; Conservative 0; Mismatches 90; Indels 3; Gaps 1;

Qy 1693 CTGGATGACCGGTCAAGGCCATCCTCTTCTCCATGCGCAGACTCGACAGGGTGAAGAAC 1752
Db 4524 CTGAAGACAAAGAAAGCGCGATCACTTCTCGATGCGCGTCTCGACCGCGTGAAGAAC 4583
Qy 1753 ATACAGGGGTGCTCGAAGCTTTTGTAACTGCGCTAAGCTGAGGAGCTGGTAAACCTT 1812
Db 4584 ATGACAGGCTGCTCGAGATGTAAGCAAGAACCGCGCTGAGGAGCTGGCGAACCTC 4643
Qy 1813 GTGCTGTTCCCGGGTACAATGATGTCAACAAGTCCAAAGACAGGGAAGAGATCGCGGAG 1872
Db 4644 GTGATGTTGCCGGTGAC---CAAGCAAGAGTCCAAAGACAGGAGGAGGAGCGCGAG 4700
Qy 1873 ATAGAGAAGATGATGAATCACTCATCAAGACCCCAACTTTTTCGGCAGTTCCCGCTGATC 1932
Db 4701 TTCAAGAAGATGATGACGCTTCATCGACGAGTACAAGTTAAGGGGCCATATCCCGTGGATC 4760
Qy 1933 TCTGCCCAGACAAACAGCGGCCCGTAAACGGCGAGCTCTATCGCTACATCGCTGTATACCCAT 1992
Db 4761 TCGGCGCAGATGAACCGCGTCCGCAACGGGAGCTGTACGCTACATTTTCGATACGAG 4820
Qy 1993 GGTGCTTTGTCAG 2007
Db 4821 GGCGCATTCGTGCAG 4835

```
RESULT 6
US-09-598-401C-56
; Sequence 56, Application US/09598401C
; Patent No. 6596325
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C2
; CURRENT APPLICATION NUMBER: US/09/598.401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 80/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Pas-Seq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-598-401C-56

Query Match      5.2%; Score 142; DB 4; Length 532;
Best Local Similarity 61.2%; Pred. No. 1.7e-26;
Matches 229; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 1 ATGCTCGCCCGAGCTGACCGCAACGCGAGCATCCGGACCGGTCGAGGACACCCCTC 60
Db 158 ATGCTGATCGCATGTTGACTCGAAGCACACGCTTCGCGAGCGTTTGGACGAGACCCCTC 217

QY 61 CACGCGCACCGCAACGAGCTCGTCCGCTCTCCAAAGTACGTGAACAGGGGAAGGC 120
Db 218 TCTGCTCACCGCAAGATATGTGCTCTCTTCAAGGTTTGAAGCCAGGGCAAGGC 277

QY 121 ATCTGACGCGGACCAATCCTGACGCGCTCGACGAGGTCGAGGGCTCCGGGGTCGCG 180
Db 278 ATCTGACGCGGACCAATCCTGAGTTTGTGCTGAGTTGAGGCTCTCTGAGGAGCAGACA 337

QY 181 GCGCTCGCGGAGGACCTCTCTGAGCTCTCTGCTCCGCGAGGAGTTTGGAGTACGTCCGCTG 240
Db 338 AGCTTCTGATGGGCTTTGTGTAAGTCTCTAAATCCACTCAGGAGGATTTGTGTCG 397

QY 241 CCGCGCTTCGTGGCCATCGCGGTGCGCCCGCGCGCGGAGTTTGGAGTACGTCCGCTG 300
Db 398 CTTCCATGGGTTGCTTGTGTTGCTTCCAAAGCGCGCGCGTGGGAGCACATCGGTG 457

QY 301 AAGCTTCACAGCTCAGCTGCGAGCAGCTCACAGTCTCGGAGTACCTTCGCTCAAGAG 360
Db 458 AAGCTTCATCGCTTGTCTTGAGCAATGAGGTTGCTGAGTATCTGCACTTCAAGAA 517

QY 361 GAGCTTGTGACGG 374
Db 518 GAGCTTGTGATGG 531

RESULT 7
US-09-313-294A-1221
; Sequence 1221, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
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; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1221
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550572H1
US-09-313-294A-1221

Query Match      4.3%; Score 117.2; DB 4; Length 272;
Best Local Similarity 67.0%; Pred. No. 2.4e-20;
Matches 181; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 1466 ATACTGTGGACAGTATGAGAGTCACTACTGCTTTACTCTGCTGCTGCTGACCGAGTTG 1525
Db 4 ACACCGTGGGCGAGTACGAGTCCCAATCGCGTTCACCTCTCTCTGCTCTACCGTGTG 63

QY 1526 TCCATGGGATCGATGCTCTTCGATCCAAAGTTCAATATAGTCTCTCTGAGCTGACATGT 1585
Db 64 TCCATGGCATCGATGTTTTCGATCCAAAGTTCAACATTTGCTCTCCCTCGAGCAGACATGA 123

QY 1586 CCATATACTTTCCCATACCGAGAGGCAAGCGACTCACCTCTCTTCATGTTCAATCG 1645
Db 124 GTGTTTACTACCGTATACGGA-AACGACAGAGACTCACTGCTTCCATCTCTGAAATCG 182

QY 1646 AAAATTGATTTATGACCCCGAGCAAAACGATGAACACATTGGGCTCTGATGACCGGT 1705
Db 183 AGGAGCTCATCTACAGCGAGCTCGAGAACTCCGAGCACAAGTTCTGCTGAAGGACAAGA 242

QY 1706 CAAAGCCCATCTCTTCTCCATGGCAAGAC 1735
Db 243 AGAAGCCGATCATCTTCTCGATGGCGGTC 272

RESULT 8
US-09-313-294A-1826
; Sequence 1826, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1826
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551585H1
US-09-313-294A-1826

Query Match      4.1%; Score 111.8; DB 4; Length 271;
Best Local Similarity 65.7%; Pred. No. 5.7e-19;
Matches 178; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

QY 889 CCGACACAGGAGCAGATCGTCTATATCTGACCAAGTCCGTGCACTAGAAAATGAG 948
Db 2 CCGACACCGGAGCGCAGGTTGCTACATCTTGATCAAGTGGCGGCTCTCGAGAACGAA 61

QY 949 ATGTTCTTCGTTTAAAGAAACAGGCTTGATGTTTCCCAAGATCTCTATTGTTACT 1008
Db 62 ATGCTGCTGAGGATCAAGCAGTGTGGTCTTGACATCGCGGAGAGTCTTATTGTACCC 121

QY 1009 CGGCTGATACAGATGCAAAAGGAACATCATGCAATCAGCGGCTTGAGAGAAATAGTGA 1068
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Db 122 AGTTGCTCCCTGATGCACTGGCCACCACCTGTGGCCAGCCCTTGAGAAAGTCTCTGGC 181
QY 1069 ACACAGCATACTTACATATTACGAGTTCCTTCAGAAATGAAATGGATCTTAAGAA 1128
Db 182 AC-CGGCACTGCCATATCTTCGGTGTGCACTCAGAACAGAAACGGGAATCGTTGGCA 240
QY 1129 TGGATATCAAGATTGTATGTGTGCCATATC 1159
Db 241 TGGATCTCGCATTTGAAGTCTGGCCGTACC 271

RESULT 9
US-08-175-471-6
; Sequence 6, Application US/08175471
; Patent No. 5665892
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J.M.
; APPLICANT: Voelker, T.
; TITLE OF INVENTION: Sucrase Phosphate Synthase (SPS), Its
; TITLE OF INVENTION: Process For Preparation, Its cDNA, and Utilization of cDNA To
; TITLE OF INVENTION: Modify The Expression Of SPS In The Plant Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,471
; FILING DATE: 27-DEC-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/672,646
; FILING DATE: 18 MAR 1991
; APPLICATION NUMBER: EP 90402084.9
; FILING DATE: 20 JUL 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 72-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-175-471-6

Query Match 3.3%; Score 89.8; DB 1; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTTGGCATCTGATGACCGGTCAAGCCCATCTTCTTCCATGGCAAGACTC 1737
Db 1543 GAAAGTATCGGTTCCTGACCAACCTCAAGCCCATGATCTGCGTTATCAAGACCA 1602
QY 1738 GACAGGGTGAAGACATACAGGGTGTGGAAGCTTTTGTAAGTGCCTTAGCTGAGG 1797

Db 1603 GACCCGAGAGACATACACTACCTCTGTCAAGGTTTGGAGAGTGTGCTCCACTCAGG 1662
QY 1798 GAGCTGGTAAACCTTGTCTGTTGCCGGGTACAAATGATGTCAAAAGTCCAAAGCAGG 1857
Db 1663 GAACTTGCMAACCTTACTCTGATCATGGTTAAACAGAGATGACATCGACGACATGTCTCT 1722
QY 1858 GAAGAGATCGCGAGTAGAAGATGATGATCAATCTCAAGACCCCAACACTTGTTCGGG 1917
Db 1723 GGCAATGCCAGTGTCTCCACACAGTTCGTAAGCTGATTGCAAGTATGATCTGTACCG- 1781
QY 1918 CAGTTCCGCTGGATCTCTGCCCCAGACAAACAGGGCCCCGTAACGGGAGCTCTATCGCTAC 1977
Db 1782 --AAGCTGGCGTTCCCTTAGCATCAATCAGGCTGACGTCCTCCGAGATCTATCGCTC 1839
QY 1978 ATCGCTGATACCCATGGTGTCTTCTGTCAGCGCGGCTTGTATGAAGCGTTTGGTCTCACC 2037
Db 1840 GCGGCCAAATGAAGGGCGTCTTCATCAACCTGCTCTGCTGAGCCGCTTTGGTCTCACC 1899
QY 2038 GTCGTTGAGGCCAATGACCTGTGGGCTTCTCTACTTTTCGGAGCGCTCCATGGAGTCCAGCT 2097
Db 1900 CTGATCGAGGCTGCGGCACACGAGTCTCCGATAGTCTGCTACCAAGATGGTGGTCCGCTC 1959
QY 2098 GAGATCATAGACATGGCGTCTCGGGCTTCCACATTTGACCGGTACCCACC 2146
Db 1960 GACATTACAAATGCATTAAACACGAGTCTGCTGTGACCCACACGACC 2008

RESULT 10
US-08-718-777-6
; Sequence 6, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Voelker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: PHOSPHATE IN PLANTS
; TITLE OF INVENTION: SYNTHASE IN PLANTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Barbara Rae-Venter
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,777
; FILING DATE: NOT YET ASSIGNED
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,471
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.072.020S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear


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; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 112..3315
; US-08-718-777-5

Query Match      3.3%; Score 89.8; DB 2; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTGGGCATCTGGATGACCGGTCAAGGCCCATCTCTTCTCCATGGCAGACATC 1737
Db 1543 GAAGTGATGCGGTCTCTGACCAACCTCTCAAGCCGATGATCTCTGGCGTTATCAAGACCA 1602
QY 1738 GACAGGTGAAGAAATACAGGGGTGTCGAAGCTTTTGTAACTGCGCTAAGCTGAGG 1797
Db 1603 GACCCGAAGAAGAACATCACTACCTCTGCAAGCTTTGGAGAGTGTCTCCACTCAGG 1662
QY 1798 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1857
Db 1663 GAACCTTGAAAACCTTACTCTGATCATGCGGTAAACAGAGATGACATCGACATGCTGCT 1722
QY 1858 GAAGAGATCGCGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1917
Db 1723 GGCATGCGCAGTCTCTCAACACAGTCTGATGATGATGATGATGATGATGATGATGATGAT 1781
QY 1918 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1977
Db 1781 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1839
QY 1978 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 2037
Db 1839 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1899
QY 2038 GTCGTTGAGGCGCATGCTGTTGGGCTTCTACTTTCGCGAGCTCCATGGAGTCCAGCT 2097
Db 1899 GTCGTTGAGGCGCATGCTGTTGGGCTTCTACTTTCGCGAGCTCCATGGAGTCCAGCT 1959
QY 2098 GAGATCATAGAGCATGGCGTCTCGGGCTTCCACATGACCGGTACCC 2146
Db 1959 GAGATCATAGAGCATGGCGTCTCGGGCTTCCACATGACCGGTACCC 2008

RESULT 11
US-09-078-862-2
; Sequence 2, Application US/09078862
; Patent No. 6091003
; GENERAL INFORMATION:
; APPLICANT: Nan, Guo-Ling
; APPLICANT: Nagai, Chifumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
; TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,862
; FILING DATE: 14-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UH-03321

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-078-862-2

Query Match      3.3%; Score 89.8; DB 3; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTGGGCATCTGGATGACCGGTCAAGGCCCATCTCTTCTCCATGGCAGACATC 1737
Db 1543 GAAGTGATGCGGTCTCTGACCAACCTCTCAAGCCGATGATCTCTGGCGTTATCAAGACCA 1602
QY 1738 GACAGGTGAAGAAATACAGGGGTGTCGAAGCTTTTGTAACTGCGCTAAGCTGAGG 1797
Db 1603 GACCCGAAGAAGAACATCACTACCTCTGCAAGCTTTGGAGAGTGTCTCCACTCAGG 1662
QY 1798 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1857
Db 1663 GAACCTTGAAAACCTTACTCTGATCATGCGGTAAACAGAGATGACATCGACATGCTGCT 1722
QY 1858 GAAGAGATCGCGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1917
Db 1723 GGCATGCGCAGTCTCTCAACACAGTCTGATGATGATGATGATGATGATGATGATGATGAT 1781
QY 1918 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1977
Db 1781 GAGCTGTAAACCTTGTCTGTTCCCGGGTACAATGATGTCACAAAGTCCAGGACAGG 1839
QY 1978 ATCGCTGATACCCATGCTTTCGTACAGCGGCTTGTATGATGATGATGATGATGATGATGAT 2037
Db 1839 ATCGCTGATACCCATGCTTTCGTACAGCGGCTTGTATGATGATGATGATGATGATGATGATGAT 1899
QY 2038 GTCGTTGAGGCGCATGCTGTTGGGCTTCTACTTTCGCGAGCTCCATGGAGTCCAGCT 2097
Db 1899 GTCGTTGAGGCGCATGCTGTTGGGCTTCTACTTTCGCGAGCTCCATGGAGTCCAGCT 1959
QY 2098 GAGATCATAGAGCATGGCGTCTCGGGCTTCCACATGACCGGTACCC 2146
Db 1959 GAGATCATAGAGCATGGCGTCTCGGGCTTCCACATGACCGGTACCC 2008

RESULT 12
US-09-051-341-6
; Sequence 6, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:

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Job time : 136.484 secs

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Db	1782	--AAGCGTGGCGTTCCCTAAGCATCAATCAGGCTGACGTCCCGGAGATCTATCGCCTC	1839
Qy	1978	ATCGCTGATACCAAGTGTGCTTTTCGTACAGCCGGCCCTTGATGAAGGGTTCGCTCTCAAC	2037
Db	1840	CGCGCAAAATGAAGGCGTCTTCATCAACCTGCTCTCGTTGAGCCGTTTGCTCTCAAC	1899
Qy	2038	GTGCTTGAGGCCAATGACCTGTGGCTTCTCTACTTTTCGGACCGTCCCATGAGAGTCCAG	2095
Db	1900	CTGATCGAGCTCGGSCACACGACCTCCCGATAGTCGTACCAAGAAATGCTGTGTCGG	1957

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:31:02 ; Search time 689.979 Seconds
(without alignments)
16851.697 Million cell updates/sec

Title: US-10-080-114A-1
Perfect score: 2737
Sequence: 1 gtagccaccgctccgcccgc.....aaaaaaaaaaggcggccgc 2737

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 3373863 seqs, 2124099041 residues
Word size : 50

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: geneseqn2001as: *
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8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2737	100.0	2737	6	Aad45849 Corn suc
2	2571	93.9	2757	6	Aad45856 Corn suc
3	278	10.2	428	8	Aad58861 Maize suc
4	255	9.3	303	8	Aad58379 Maize suc
5	209	7.6	283	8	Aad58372 Maize suc
6	192	7.0	297	9	Adc08886 Corn DNA
7	191	7.0	258	9	Adc08843 Corn DNA
8	159	5.8	285	8	Aad58359 Maize suc
9	158	5.8	297	8	Aad58362 Maize suc
10	150	5.5	150	8	Ada58373 Maize suc
11	143	5.2	411	8	Ada58864 Maize suc
12	134	4.9	255	8	Ada58374 Maize suc
13	130	4.7	181	8	Ada58370 Maize suc
14	122	4.5	265	7	Abx83402 Corn ear-
15	114	4.2	310	8	Ada58369 Maize suc
16	99	3.6	148	8	Ada58371 Maize suc
17	85	3.1	347	6	Aad45857 Sorghum p
18	83	3.0	137	8	Ada58375 Maize suc
19	63	2.3	264	8	Aad58368 Maize suc

ALIGNMENTS

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RESULT 1
AAD45849
ID AAD45849 standard; cDNA; 2737 BP.
XX
AC AAD45849;
XX
DT 27-DEC-2002 (first entry)
XX
DE Corn sucrose synthase (Sus3) cDNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
cellulose; corn; Sus3; gene; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
CDS 2..2410
FT /*tag= a
FT /product= "Corn Sus3 protein"
XX
PN WO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
XX
XX WPI; 2002-691625/74.
XX
XX P-PSDB; AAE28499.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
modulating the level of sucrose synthase in transgenic plants (e.g. maize
or soybean) to improve stalk length, reduce grain breakage, or improving
plant or grain strength.
XX
XX Claim 1; Page 102-103; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
constitutive sucrose synthase (Sus1) and their corresponding nucleic
acids. The polynucleotide, or its encoded protein, is useful for
modulating the level of sucrose synthase in a transgenic plant,
increasing cellulose production in the stalk tissue of a transgenic
plant, or increasing the concentration of cellulose in the tissues of a
seed of a transgenic plant. This is particularly useful in plant (e.g.
maize or soybean) breeding, especially for e.g. improving stalk length in
maize, reducing grain breakage during combining, transport or movement
into storage, or improving plant or grain strength. The present sequence
is corn Sus3 cDNA
XX
SQ Sequence 2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2737; DB 6; Length 2737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGACCCACGCTCCGGCCGCGGACCGGTCGAGGACACCTCCACGCGCACCGACGAGCT 60
Db 1 GTGACCCACGCTCCGGCCGCGGACCGGTCGAGGACACCTCCACGCGCACCGACGAGCT 60
Qy 61 CGTGGCCCTCTGTCCCAAGTACGTGAACAGGGGAAAGGGCATCTTCGAGCCGACCAAT 120
Db 61 CGTGGCCCTCTGTCCCAAGTACGTGAACAGGGGAAAGGGCATCTTCGAGCCGACCAAT 120
Qy 121 CCTGACGCGCTCGACGAGGTCCAGGGGCTCCGGGGGGCGCGCTAGCCGAGGACCTT 180
Db 121 CCTGACGCGCTCGACGAGGTCCAGGGGCTCCGGGGGGCGCGCTAGCCGAGGACCTT 180
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181 QY CCTCGAGCTCCTCCGCTCGCGCAGGAGGCGATCGTGTGCGGCCGCTTGGTGGCCATCGC 240
181 DB CCTCGAGCTCCTCCGCTCGCGCAGGAGGCGATCGTGTGCGGCCGCTTGGTGGCCATCGC 240
241 QY GGTGCGCCGCGCGCCGGGAGTTGGAGTAGCTGCGCGCTCAAGCTTCACGAGCTCAGCGT 300
241 DB GGTGCGCCGCGCGCCGGGAGTTGGAGTAGCTGCGCGCTCAAGCTTCACGAGCTCAGCGT 300
301 QY CGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTGTGTGCGAGCGCCAGCA 360
301 DB CGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTGTGTGCGAGCGCCAGCA 360
361 QY CAATGATCCCTAGCTTCTCGAGCTTCACTTCGAGCCGCTTCAATGTCTCAGTCCCAAGCC 420
361 DB CAATGATCCCTAGCTTCTCGAGCTTCACTTCGAGCCGCTTCAATGTCTCAGTCCCAAGCC 420
421 QY AAATCGGTCATCATCTATTGGAAACGGTGTGCAGTTCCTCAACCGGACACTTGTCTCTCAAT 480
421 DB AAATCGGTCATCATCTATTGGAAACGGTGTGCAGTTCCTCAACCGGACACTTGTCTCTCAAT 480
481 QY CATGTTCCGGAACAGGAGTGTGTGAGCCGCTGTGAGTTTCTCCGTGGGCCACCGGCA 540
481 DB CATGTTCCGGAACAGGAGTGTGTGAGCCGCTGTGAGTTTCTCCGTGGGCCACCGGCA 540
541 QY CAAGGGCATGTATGATGCTTAACTGATAGATACAAAGCTTGGGAGGCTTCAGTCTGT 600
541 DB CAAGGGCATGTATGATGCTTAACTGATAGATACAAAGCTTGGGAGGCTTCAGTCTGT 600
601 QY GCTGACAAAGCTGAGGAGCACTGTCAAGCTCCCTGTGTGATGATGATGATGATGATGAT 660
601 DB GCTGACAAAGCTGAGGAGCACTGTCAAGCTCCCTGTGTGATGATGATGATGATGATGAT 660
661 QY TGTCTATAAATTTCAAGAGTGGGCTCGGAGAAAGTGTGGGGTGAACACAGGAGCAATGT 720
661 DB TGTCTATAAATTTCAAGAGTGGGCTCGGAGAAAGTGTGGGGTGAACACAGGAGCAATGT 720
721 QY TTGTGAAATGATCCATCTCTCTAGACATCATTCAGGCGCCAGACCCATCTACCCCTAG 780
721 DB TTGTGAAATGATCCATCTCTCTAGACATCATTCAGGCGCCAGACCCATCTACCCCTAG 780
781 QY GAAATTTCTGGGAGGATCCCATGATTTTAACTGTTGTGATGATGATGATGATGATGATGAT 840
781 DB GAAATTTCTGGGAGGATCCCATGATTTTAACTGTTGTGATGATGATGATGATGATGATGAT 840
841 QY CTTTGGTCAAGCTTAATGATTAAGCTTGCAGACACAGGAGGACAGATCGTCTATATACT 900
841 DB CTTTGGTCAAGCTTAATGATTAAGCTTGCAGACACAGGAGGACAGATCGTCTATATACT 900
901 QY GGACCAAGTCCGTGCACTAGAAAAAGATGATGTTCTCCGTTTAAAGAAACAGGGCTTGA 960
901 DB GGACCAAGTCCGTGCACTAGAAAAAGATGATGTTCTCCGTTTAAAGAAACAGGGCTTGA 960
961 QY TGTTCCTCCAAAGATTTCTCATTTTACTCGGCTGATACAGATGCAAAAGGAAACATCATG 1020
961 DB TGTTCCTCCAAAGATTTCTCATTTTACTCGGCTGATACAGATGCAAAAGGAAACATCATG 1020
1021 QY CAATCAGCGGCTTGAGAGAAATAGTGGAAACACAGCATCTTACATTAATGAGTTCCCTT 1080
1021 DB CAATCAGCGGCTTGAGAGAAATAGTGGAAACACAGCATCTTACATTAATGAGTTCCCTT 1080
1081 QY CAGAAATGAAATGGGATACCTTAAAGAAATGGATATCAAGATTTGATGTGGCCATATCT 1140
1081 DB CAGAAATGAAATGGGATACCTTAAAGAAATGGATATCAAGATTTGATGTGGCCATATCT 1140
1141 QY GGAACATTTGTGAGAGATGCTGCTGGTGAATGCTGTGAATTAAGAGTACTCCAGA 1200
1141 DB GGAACATTTGTGAGAGATGCTGCTGGTGAATGCTGTGAATTAAGAGTACTCCAGA 1200
1201 QY CTTTCAATTTGAAACACAGTATGGAATCTTGTGGGCTGATGCTATCTTACAGAT 1260
1201 DB CTTTCAATTTGAAACACAGTATGGAATCTTGTGGGCTGATGCTATCTTACAGAT 1260

1261 QY GGAATTTACCCAGTCAACATTCCTCATCTCTGGAAGAGACTAAGTATCCAGATTGAGA 1320
1261 DB GGAATTTACCCAGTCAACATTCCTCATCTCTGGAAGAGACTAAGTATCCAGATTGAGA 1320
1321 QY CATATTTTGAAGAAATTTCCGATGAGAGTACCAATTTCTCTGCGAGTTCATCTGTATAT 1380
1321 DB CATATTTTGAAGAAATTTCCGATGAGAGTACCAATTTCTCTGCGAGTTCATCTGTATAT 1380
1381 QY AATTGCTATGAAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTTGCTGAAG 1440
1381 DB AATTGCTATGAAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTTGCTGAAG 1440
1441 QY CAAATATCTGTTGGACAGTATGAGAGTACATCTGCTTTTACITCTGCTGGTCTGTACCG 1500
1441 DB CAAATATCTGTTGGACAGTATGAGAGTACATCTGCTTTTACITCTGCTGGTCTGTACCG 1500
1501 QY AGTTGTCCATGGATCGATGTCTTTCGATCCAAAGTTCAATATAGTCTCTCTGGAGCTGA 1560
1501 DB AGTTGTCCATGGATCGATGTCTTTCGATCCAAAGTTCAATATAGTCTCTCTGGAGCTGA 1560
1561 QY CATGTCATATATCTTTCCACATACCGAGAGGCGCAAGGACTCACTCTCTCTCATGTTTC 1620
1561 DB CATGTCATATATCTTTCCACATACCGAGAGGCGCAAGGACTCACTCTCTCTCATGTTTC 1620
1621 QY AATCGAAATTTGATTTATGACCCGAGCAAAACGATGAACATTTGGGCTCTGTGATGA 1680
1621 DB AATCGAAATTTGATTTATGACCCGAGCAAAACGATGAACATTTGGGCTCTGTGATGA 1680
1681 QY CCGGTCAAAGCCCATCTCTTCTCCATGSCAAGACTCGACAGGCTGAAGAACATAACAGG 1740
1681 DB CCGGTCAAAGCCCATCTCTTCTCCATGSCAAGACTCGACAGGCTGAAGAACATAACAGG 1740
1741 QY GCTGTCGAAGCTTTTGTCTTAAGTCGCTTAAGCTGAAGGAGCTGCTGATAAACCCTGTGCTGT 1800
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1861 DB GATGCTGAATCAATCAAGACCAACTTGTTCGGGCGAGTTCGCTGGATCTCTGCCCA 1920
1921 QY GACAAACAGGCGCCGTAAAGGCGAGCTTATGCTGCTGATGCTGATACCACTGCTGCTTT 1980
1921 DB GACAAACAGGCGCCGTAAAGGCGAGCTTATGCTGCTGATGCTGATACCACTGCTGCTTT 1980
1981 QY CGTACAGCGCGCTTGTATGAGCGTTCCGCTCTCACCGCTTGGGCGCATGACCTGTGG 2040
1981 DB CGTACAGCGCGCTTGTATGAGCGTTCCGCTCTCACCGCTTGGGCGCATGACCTGTGG 2040
2041 QY GCTTCTTCTTTCGCGACGCTCCATGAGGCTCCAGCTGAGATCATAGAGCATGGCGTCTC 2100
2041 DB GCTTCTTCTTTCGCGACGCTCCATGAGGCTCCAGCTGAGATCATAGAGCATGGCGTCTC 2100
2101 QY GGGCTTCCATTTGACCCGCTTACCCCGAAACGCTGCTGATGCTGATGCTGCTGCTGCT 2160
2101 DB GGGCTTCCATTTGACCCGCTTACCCCGAAACGCTGCTGATGCTGATGCTGCTGCTGCT 2160
2161 QY CGACCGGTCGAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAGAGGCGCTGCAGCG 2220
2161 DB CGACCGGTCGAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAGAGGCGCTGCAGCG 2220
2221 QY CATATACGAGAGATACATCATGGAAGATATCTCAGAGAGGTTGATGATCACTGCGCGGCT 2280
2221 DB CATATACGAGAGATACATCATGGAAGATATCTCAGAGAGGTTGATGATCACTGCGCGGCT 2280
2281 QY CTACGCTTTCTGGAAGTACGTGTCGAAGCTCGAGAGGCTGGAGACGAGGCGCTACCTTGA 2340
2281 DB CTACGCTTTCTGGAAGTACGTGTCGAAGCTCGAGAGGCTGGAGACGAGGCGCTACCTTGA 2340
2341 QY GATGTTCTATACATCTGAGTTCGCGAGCTGGCGAAGACCGTGCCTTGAATTGACCA 2400

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Db 2341 GATCTTCTACACTAGATTCGCGAGCTGGCGAAGCGTGCCTTGCAATGACCA 2400
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Db 2401 ACCGAGTAGCTTGGCAACTGGCACTGGCTAGCACTGGTGTACAAAGCTGAAG 2460
QY 2461 GACCTTCAGTAATTTAGCGCGGCGGAGCGGTAGCAATAAATGTGCGGAGCTGAAG 2520
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QY 2521 GTTTTATTATGTACATAATGCGAGTATACAAATAAATCTGAAGGAGGTGGTTCAG 2580
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QY 2641 GCAAGCGGAGGAGCTGCTGAAGTCTGATCAATATACATCATATTTCTGTTGACCTGTGAA 2700
Db 2641 GCAAGCGGAGGAGCTGCTGAAGTCTGATCAATATACATCATATTTCTGTTGACCTGTGAA 2700
QY 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGC 2737
Db 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGC 2737

RESULT 2
AAD45856
ID AAD45856 standard; DNA; 2757 BP.
AC AAD45856;
XX
DT 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
XX
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; chimeric; gene; ds.
XX
OS Zea mays.
OS Sorghum propinquum.
OS Chimeric.
XX
Key Location/Qualifiers
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FT misc_feature 40..2757
FT /*tag= c
FT /note= "Corn Sus3 DNA"
XX
PN WO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
XX
XX NPI; 2002-691625/74.
XX
XX P-PSDB; AAE28502.
XX

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PT New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.
XX
PS Claim 1; Page 116-119; 125pp; English.
XX
CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
CC acids. The polynucleotide, or its encoded protein, is useful for
CC modulating the level of sucrose synthase in a transgenic plant,
CC increasing cellulose production in the stalk tissue of a transgenic
CC plant or increasing the concentration of cellulose in the tissues of a
CC seed of a transgenic plant. This is particularly useful in plant (e.g.
CC maize or soybean) breeding, especially for e.g. improving stalk length in
CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is Corn Sus3-Sorghum EST chimeric DNA. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;

Query Match          93.9%; Score 2571; DB 6; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GCCGAGGACCCCTTCCTCGACGCTCCTCGCTCCGCGGCGGAGGCGGATCGTCTGCCGCG 226
Db 187 GCCGAGGACCCCTTCCTCGACGCTCCTCGCTCCGCGGCGGAGGCGGATCGTCTGCCGCG 246
QY 227 TTCTGTGCGCATCGCGGTGCGCGCGCGCGGAGTTTGGGAGTAGCTCGCGGTCAACGTT 286
Db 247 TTCTGTGCGCATCGCGGTGCGCGCGCGCGGAGTTTGGGAGTAGCTCGCGGTCAACGTT 306
QY 287 CACGAGCTCAGCGTCTGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTT 346
Db 307 CACGAGCTCAGCGTCTGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTT 366
QY 347 GTGAGCGGCGAGCAATGATCCCTACGTTCTGAGCTTGACTTCGAGCGGTTCAATGTC 406
Db 367 GTGAGCGGCGAGCAATGATCCCTACGTTCTGAGCTTGACTTCGAGCGGTTCAATGTC 426
QY 407 TCAGTCCACGCCCAATCGGTCTATCTATTTGAAACGGTGTGTCAGTCTCTCAACCGA 466
Db 427 TCAGTCCACGCCCAATCGGTCTATCTATTTGAAACGGTGTGTCAGTCTCTCAACCGA 486
QY 467 CACTTGTCTCAATCATGTTCCGCAACAGGAGTTCCTTGGAGCCCTGTGGAATTCCTC 526
Db 487 CACTTGTCTCAATCATGTTCCGCAACAGGAGTTCCTTGGAGCCCTGTGGAATTCCTC 546
QY 527 CGTGGCCACCGGCGCAAGGGCGCATGTTATGATGCTTATGATAGATACAAAGCTTGGG 586
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QY 587 AGGCTTCAGTCTGTGCTGACCAAAAGCTGAGGAGCACTTGTCAAAAGCTCCCTGCTCACA 646
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QY 647 CCATACCTCACAATTTGCTTTATAAATTTTCAAGTGGGGCGCTGGAGAAAGGTTGGGCTGAT 706
Db 667 CCATACCTCACAATTTGCTTTATAAATTTTCAAGTGGGGCGCTGGAGAAAGGTTGGGCTGAT 726
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Db 727 ACAGGAGCATGTTTGGAAATGATCCATCTCTCTCTAGACATCATTCAGGCGGCGAGAC 786
QY 767 CCATCTACCTTAGAGAAATCTTCCGGGAGGATCCCATGATTTTAAAGTGTGTTGTTGTA 826
Db 787 CCATCTACCTTAGAGAAATCTTCCGGGAGGATCCCATGATTTTAAAGTGTGTTGTTGTA 846
QY 827 TCCCTCATGATACCTTTGGTCAAGCTAAATGATTTAGGCTTCCAGACACACAGGAGGACAG 886
Db 847 TCCCTCATGATACCTTTGGTCAAGCTAAATGATTTAGGCTTCCAGACACACAGGAGGACAG 906

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QY	887	ATCGTCTATATATCTGGACCAAGTCCGTFGCATAGAAAATGAGATGGTTCTCCGTTTAAAG	948
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QY	947	AAACAGGGGCTTGATGTTTCCCAAAGATTTCTANTTGTCTTACTCGGCTGATACCAGATGCA	1006
Db	967	AAACAGGGGCTTGATGTTTCCCAAAGATTTCTANTTGTCTTACTCGGCTGATACCAGATGCA	1026
QY	1007	AAAGGAACATCATGCAATTCAGCGGCTTGAGAGAAATAGTGGAAACACAGCATATTTACATA	1066
Db	1027	AAAGGAACATCATGCAATTCAGCGGCTTGAGAGAAATAGTGGAAACACAGCATATTTACATA	1086
QY	1067	TTACGAGTTCCTTTACAAATGAATGGCATCTACTTAAGAAATGGAATATCAAGATTGAT	1126
Db	1087	TTACGAGTTCCTTTACAAATGAATGGGATCTTAAAGAAATGGATATCAAGATTGAT	1146
QY	1127	GTGTGGCCATATCTGGAAAACATTTGCTTGAGAGATGCTGCTGGTGAATTCGTGGAATTA	1186
Db	1147	GTGTGGCCATATCTGGAAAACATTTGCTTGAGGATGCTGCTGGTGAATTCGTGGAATTA	1206
QY	1187	CAAGGTACTCCAGACTTCATAATTTGGAAATCCTACAGTGATGGAAATCTTGTGGCGTCAATTG	1246
Db	1207	CAAGGTACTCCAGACTTCATAATTTGGAAATCCTACAGTGATGGAAATCTTGTGGCGTCAATTG	1266
QY	1247	CTATCTTACAAGATGGGAATTTACCAGTGCACAACTTGCTCATGCTCTGGAAAAAGACTAAG	1306
Db	1267	CTATCTTACAAGATGGGAATTTACCAGTGCACAACTTGCTCATGCTCTGGAAAAAGACTAAG	1326
QY	1307	TATCCAGATTCAGACATATTTTCCGAGAAATTTCCGATGAGAAATCAATTTCTCTGCGCAG	1366
Db	1327	TATCCAGATTCAGACATATTTTCCGAGAAATTTCCGATGAGAAATCAATTTCTCTGCGCAG	1386
QY	1367	TTCACTGCTGATACATATGCTATGAAACAATGCTGATTTATCATCACCCAGCATACCAA	1426
Db	1387	TTCACTGCTGATACATATGCTATGAAACAATGCTGATTTATCATCACCCAGCATACCAA	1446
QY	1427	GAAATTCCTGGAAAGCAAAATATCTGTTGGACAGTATGAGAGTCATATCGCTTTTACTCTG	1486
Db	1447	GAAATTCCTGGAAAGCAAAATATCTGTTGGACAGTATGAGAGTCATATCGCTTTTACTCTG	1506
QY	1487	CCGCGTCTGACCGAGTGTCCATGGATGCAATGCTTCGATCCAAAGTTCAATATAGTC	1546
Db	1507	CCGCGTCTGACCGAGTGTCCATGGATGCAATGCTTCGATCCAAAGTTCAATATAGTC	1566
QY	1547	TCCTCTGGAGTCGACATGTCATATATCTTCCACATACCGAGAGGCCAAGCCACTCAC	1606
Db	1567	TCCTCTGGAGTCGACATGTCATATATCTTCCACATACCGAGAGGCCAAGCCACTCAC	1626
QY	1607	TCTCTTCATGCTCAATCGAAAATTTGATTTGACCCGGAGCAAAAGATGAACACATT	1666
Db	1627	TCTCTTCATGCTCAATCGAAAATTTGATTTGACCCGGAGCAAAAGATGAACACATT	1686
QY	1667	GGGCATCTGATGACCGGTCMAAGCCCATCTCTTCCATGCGCAAGACTCGACAGGGTG	1726
Db	1687	GGGCATCTGATGACCGGTCMAAGCCCATCTCTTCCATGCGCAAGACTCGACAGGGTG	1746
QY	1727	AGAAACATAACAGGGCTGCTGGAAGCTTTTGTCTAAAGCGCTAAGCTGAGGGAGCTGGTA	1786
Db	1747	AGAAACATAACAGGGCTGCTGGAAGCTTTTGTCTAAAGCGCTAAGCTGAGGGAGCTGGTA	1806
QY	1787	AACTTGTGCTGCTGCGGTTCAATGATGTCAAACAGTCCAAAGCAAGGAGAGATC	1846
Db	1807	AACTTGTGCTGCTGCGGTTCAATGATGTCAAACAGTCCAAAGCAAGGAGAGATC	1866
QY	1847	CGCGAGATGAGAAATGATGAACCTCATCAAGACCCACAACTTGTTCGGGCAAGTCCCG	1906
Db	1867	CGCGAGATGAGAAATGATGAACCTCATCAAGACCCACAACTTGTTCGGGCAAGTCCCG	1926
QY	1907	TGGATCTTGCCCAAGACAAACAGGGCCGTTAACGGGAGGCTTATCGCTACATCGCTGAT	1966
Db	1927	TGGATCTTGCCCAAGACAAACAGGGCCGTTAACGGGAGGCTTATCGCTACATCGCTGAT	1986

QY	1367	ACC	ATGGTGTCTTTCGTACAGCGGCTTGTATGAAGCGTTGGTCTCAACGTCGTTGAG	2026
DB	1387	ACC	ATGGTGTCTTTCGTACAGCGCGCTTCTGTATGAAGCGTTGGTCTCAACGTCGTTGAG	2046
QY	2027	GCC	ATGACCTGTGTGGCTTCTCTACTTTCGCGACGCTCCATCGAGGCTCCAGCTGAGATCATTA	2086
DB	2047	GCC	ATGACCTGTGTGGCTTCTCTACTTTCGCGACGCTCCATCGAGGCTCCAGCTGAGATCATTA	2106
QY	2087	GAG	CAATGGCGTCTGGGCTTCCACATTTGACCCCGTACACCCCGAACAGGCTGTTTAATCTG	2146
DB	2107	GAG	CAATGGCGTCTGGGCTTCCACATTTGACCCCGTACACCCCGAACAGGCTGTTTAATCTG	2166
QY	2147	ATG	CCCGCACTCTTCGACCGGTCCAGCAGAGCCAGATCACTCGGTGTAATATATCTGGA	2206
DB	2167	ATG	CCCGCACTCTTCGACCGGTCCAGCAGAGCCAGATCACTCGGTGTAATATATCTGGA	2226
QY	2207	GC	AGGCTCGAGCGCATATACGAAAGTACACATGGAAGATATATCTCAGAGAGGTTGATG	2266
DB	2227	GC	AGGCTCGAGCGCATATACGAGAACTACACATGGAAGATATATCTCAGAGAGGTTGATG	2286
QY	2267	AC	CTGCGCGGGTCTACGGTTTCTGGAAGTACGTGTCGAAGCTCGAGAGCTGGAGACG	2326
DB	2287	AC	CTGCGCGGGTCTACGGTTTCTGGAAGTACGTGTCGAAGCTCGAGAGGCTGGAGACG	2346
QY	2327	AGG	CGCTACCTTGAGATGTTCTACATACTCAAGTTTCGCGCAGCTGGCGAAGACCGTCCCG	2386
DB	2347	AGG	CGCTACCTTGAGATGTTCTACATACTCAAGTTTCGCGCAGCTGGCGAAGACCGTCCCG	2406
QY	2387	CTT	GCAATGACACCGCGAGTAGCTTGCACACTGGGACTGCGTAGCATTGGTACAAAG	2446
DB	2407	CTT	GCAATGACACCGCGAGTAGCTTGCACACTGGGACTGCGTAGCATTGGTACAAAG	2466
QY	2447	ACT	GAAACCTGGAAGGACCTTCAGTAAATTTAGGCGCGCAGACGCTAGCCCAATAAATGTG	2506
DB	2467	ACT	GAAACCTGGAAGGACCTTCAGTAAATTTAGGCGCGCAGACGCTAGCCCAATAAATGTG	2526
QY	2507	CCG	GAGCTGAACCTGTTTTTATATGATACATAATGSCAGTATAACAAATTTACTGAAGG	2566
DB	2527	CCG	GAGCTGAACCTGTTTTTATATGATACATAATGSCAGTATAACAAATTTACTGAAGG	2586
QY	2567	CAG	TGGTTCAGTGTGTGTTCTGCTTCTACTGTTTACTGTTATGTTATGTCACAGCTCTCGGCTG	2626
DB	2587	CAG	TGGTTCAGTGTGTGTTCTGCTTCTACTGTTTACTGTTATGTTATGTCACAGCTCTCGGCTG	2646
QY	2627	CAA	TTCTTTTGTCTGGCAAGCGCAGGCACCTGTGTCAAGTGTCTGATAAATACATCATATTCT	2686
DB	2647	CAA	TTCTTTTGTCTGGCAAGCGCAGGCACCTGTGTCAAGTGTCTGATAAATACATCATATTCT	2706
QY	2687	GTT	GACCTGTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCGC	2737
DB	2707	GTT	GACCTGTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCGC	2757
RESULT 3				
ADA58861				
ID	ADA58861 standard; cDNA; 428 BP.			
XX	ADA58861;			
XX	AC			
XX	AC			
DT	20-NOV-2003 (first entry)			
XX	Maize sucrose synthase EST #505.			
DE				
XX	Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;			
KW	triase phosphate isomerase; fructose 1; 6-bisphosphate aldolase;			
KW	fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;			
KW	phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;			
KW	pyrophosphate-dependent fructose 6-phosphate phosphotransferase;			
KW	invertase; sucrose synthase; hexokinase; fructokinase;			
KW	nucleoside diphosphate kinase-kinase; NDP;			
KW	glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;			
KW	uridine diphosphate-glucose pyrophosphorylase; maize.			


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OS XX Zea mays.
PN XX US2003135870-A1.
XX XX 17-JUL-2003.
XX PF 26-JAN-1999; 99US-00237183.
XX PR 24-NOV-1997; 97US-0067000P.
XX PR 09-DEC-1997; 97US-0069472P.
XX PR 27-JAN-1998; 98US-0072888P.
XX PR 10-FEB-1998; 98US-0074201P.
XX PR 10-FEB-1998; 98US-0074280P.
XX PR 10-FEB-1998; 98US-0074281P.
XX PR 10-FEB-1998; 98US-0074282P.
XX PR 12-FEB-1998; 98US-0074565P.
XX PR 12-FEB-1998; 98US-0074566P.
XX PR 12-FEB-1998; 98US-0074567P.
XX PR 19-FEB-1998; 98US-0074789P.
XX PR 19-FEB-1998; 98US-0075459P.
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XX PR 06-MAR-1998; 98US-0076912P.
XX PR 09-MAR-1998; 98US-0077229P.
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XX PR 29-APR-1998; 98US-0083389P.
XX PR 29-APR-1998; 98US-0083390P.
XX PR 13-MAY-1998; 98US-0085222P.
XX PR 13-MAY-1998; 98US-0085223P.
XX PR 13-MAY-1998; 98US-0085224P.
XX PR 21-MAY-1998; 98US-0086183P.
XX PR 21-MAY-1998; 98US-0086184P.
XX PR 21-MAY-1998; 98US-0086185P.
XX PR 21-MAY-1998; 98US-0086186P.
XX PR 21-MAY-1998; 98US-0086187P.
XX PR 21-MAY-1998; 98US-0086188P.
XX PR 01-JUN-1998; 98US-0087422P.
XX PR 16-JUN-1998; 98US-0089524P.
XX PR 18-JUN-1998; 98US-0089793P.
XX PR 18-JUN-1998; 98US-0089810P.
XX PR 22-JUN-1998; 98US-0090170P.
XX PR 26-JUN-1998; 98US-0090328P.
XX PR 29-JUN-1998; 98US-0091035P.
XX PR 30-JUN-1998; 98US-0091405P.
XX PR 08-JUL-1998; 98US-0092036P.
XX PR 09-SEP-1998; 98US-0099667P.
XX PR 09-SEP-1998; 98US-0099670P.
XX PR 09-SEP-1998; 98US-0099697P.
XX PR 16-SEP-1998; 98US-0100672P.
XX PR 16-SEP-1998; 98US-0100673P.
XX PR 16-SEP-1998; 98US-0100674P.
XX PR 21-SEP-1998; 98US-0101130P.
XX PR 21-SEP-1998; 98US-0101131P.
XX PR 21-SEP-1998; 98US-0101132P.
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XX PR 22-SEP-1998; 98US-0101508P.
XX PR 25-SEP-1998; 98US-0101707P.
XX PR 13-OCT-1998; 98US-0104123P.
XX PR 13-OCT-1998; 98US-0104124P.
XX PR 13-OCT-1998; 98US-3104126P.

PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX (CHEI/) CHEIKH N.
PA (FISH/) FISHER D X.
PA (LIU/) LIU J.
XX Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX New maize or soybean enzymes and nucleic acid molecules associated with
PT the sucrose pathway, useful for genome mapping, gene identification and
PT analysis, plant breeding, or preparation of constructs for plant gene
PT expression.
XX Claim 2; Page; 117pp; English.
XX The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADAM57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphatase-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: the sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20030135870.
XX Sequence 428 BP; 118 A; 95 C; 126 G; 89 T; 0 U; 0 Other;

Query Match 10.2%; Score 278; DB 8; Length 428;
Best Local Similarity 99.7%; Pred. No. 1.1e-99;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2198 ATATCTGGAGCAGGCTGCAGCGGATATACGAGAGTACACATGACATGACATATACACAG 2257
DB 63 ATATCTGGAGCAGGCTGCAGCGGATATACGAGAGTACACATGACATGACATATACACAG 122
QY 2258 AGGTTGATGACATCGCGCGGGTCTACCGTTTCTGGAAGTACGTTCTGGAAGTACGAGG 2317
DB 123 AGGTTGATGACATCGCGCGGGTCTACCGTTTCTGGAAGTACGTTCTGGAAGTACGAGG 182
QY 2318 CTGGAGACGAGCGCTACCTTGAGATGTTCTACATGAGTTCGCGAGTCGCGAGG 2377
DB 183 CCGGAGACGAGCGCTACCTTGAGATGTTCTACATGAGTTCGCGAGTCGCGAGG 242
QY 2378 ACOGTGCGCTTGCAATTGACCAACCGCAGTAGCTTGCGCACTGCGACTGCGTAGCACT 2437

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Db      303  TGGTACAAGACTGAACCTGAAGACCTTCAGTAATTTAGGCGCGCGAGACGCTAGCCAA 362
QY      2498  TAAATGTCCGCGAGCTGAACCTGTTTTT 2526
Db      363  TAAATGTCCGCGAGCTGAACCTGTTTTT 391

RESULT 4
ADA58379
ID ADA58379 standard; cDNA; 303 BP.
XX
AC ADA58379;
XX
DT 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #23.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-AL.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 99US-00237183.
XX
PR 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080848P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083386P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083389P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
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PR 16-SEP-1998; 98US-0100672P.
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PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX
(CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
PI Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX
PT New maize or soybean enzymes and nucleic acid molecules associated with
PT the sucrose pathway, useful for genome mapping, gene identification and
PT analysis, plant breeding, or preparation of constructs for plant gene
PT expression.
XX
PS Claim 2; Page; 117pp; English.
XX
CC The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern

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CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
XX
SQ Sequence 303 BP; 71 A; 78 C; 86 G; 58 T; 0 U; 0 Other;

Query Match          9.3%; Score 255; DB 8; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.3e-90;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1741 GCTGGTCAAGCTTTGCTAAGTGGCTAAGCTCAGGAGCTGCTAAACCTTGTGCTGCT 1800
Db 1 GCTGGTCAAGCTTTGCTAAGTGGCTAAGCTCAGGAGCTGCTAAACCTTGTGCTGCT 60

QY 1801 TGCGGGGTACAATGATGTCAACAAAGTCCAAAGACAGGAGAGATCGCGAGATAGAGAA 1860
Db 61 TGCGGGGTACAATGATGTCAACAAAGTCCAAAGACAGGAGAGATCGCGAGATAGAGAA 120

QY 1861 GATGCATGAAGTATCATCAAGACCCCACTTTTCGGGAGTTCGCTGGATCTCTGCCCA 1920
Db 121 GATGCATGAAGTATCATCAAGACCCCACTTTTCGGGAGTTCGCTGGATCTCTGCCCA 180

QY 1921 GACAAACAGGCGCGTAAACGCGAGCTATCGCTACATCCGCTATACCCATGCTGCTTT 1980
Db 181 GACAAACAGGCGCGTAAACGCGAGCTATCGCTACATCCGCTATACCCATGCTGCTTT 240

QY 1981 CGTACAGCGCGCTT 1995
Db 241 CGTACAGCGCGCTT 255

RESULT 5
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ID ADA58372 standard; cDNA; 283 BP.
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AC ADA58372;
XX
Df 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #16.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-A1.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 99US-00237183.
XX
PR 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
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PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083386P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
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PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
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PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
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PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
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PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108966P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX
XX (CHEI/) CHEIKH N.
XX (FISH/) FISHER D K.
XX (LIUJ/) LIU J.
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XX Cheikh N, Fisher DK, Liu J;
 XX WPI; 2003-698722/65.
 XX New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and
 PT analysis, plant breeding, or preparation of constructs for plant gene
 PT expression.
 XX
 XX Claim 2; Page; 117pp; English.
 XX
 CC The invention relates to a substantially purified nucleic acid molecule
 CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucosylomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucuronase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC transformed plant having a nucleic acid molecule. Also disclosed as new
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
 XX
 SQ Sequence 283 BP; 75 A; 74 C; 67 G; 67 T; 0 U; 0 Other;
 Query Match 7.6%; Score 209; DB 8; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1529 CCAAGTTCAATATAGTCTCTCTCGAGCTGACATGTCATATACITTCACATACCGAG 1588
 DB 9 CCAAGTTCAATATAGTCTCTCTCGAGCTGACATGTCATATACITTCACATACCGAG 68
 QY 1589 AAGGCCAAGCGACTCACCTCTCTTCATGGTTCAATCGAATTTGATTTATGACCCGGAG 1648
 DB 69 AAGGCCAAGCGACTCACCTCTCTTCATGGTTCAATCGAATTTGATTTATGACCCGGAG 129
 QY 1649 CAAACGATGAACACANTTGGGCATCTGGATGACCGGTCAAAGCCCATCTCTTCTCCATG 1708
 DB 129 CAAACGATGAACACANTTGGGCATCTGGATGACCGGTCAAAGCCCATCTCTTCTCCATG 188
 QY 1709 GCAAGACTCGACGGGTGAAGACATAAC 1737
 DB 189 GCAAGACTCGACGGGTGAAGACATAAC 217
 RESULT 6
 ADC08886/c
 ID ADC08886 standard; DNA; 297 BP.
 XX
 AC ADC08886;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Corn DNA sequence Seq ID:1.91 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 XX gene; ds; plant.
 XX
 OS Zea mays.
 XX
 PN WO2003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002WO-1B002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 28-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX
 PA (SVGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX
 DR WPI; 2003-229341/22.
 XX
 CC New plant genes encoding polypeptides having an activity involved in or
 CC associated with the synthesis, metabolism or degradation of carbohydrates
 CC in the plant grain useful in generating plants having improved
 CC nutritional properties.
 PT
 PT Disclosure; SEQ ID NO 1191; 130pp; English.
 XX
 CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence from corn which showed homology to rice "grain filling"
 CC genes of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
 XX
 SQ Sequence 297 BP; 87 A; 57 C; 70 G; 83 T; 0 U; 0 Other;
 Query Match 7.0%; Score 192; DB 9; Length 297;
 Best Local Similarity 99.6%; Pred. No. 9.2e-66;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1373 GCTGATATATTTGCTATGAACATGCTGATTTATCATCATCAGCACATACAGAAATT 1432
 DB 243 GCTGATATATTTGCTATGAACATGCTGATTTATCATCATCAGCACATACAGAAATC 184
 QY 1433 GCTGGAAGCAAAATATCTGTTGGACATGATGAGATCATCTGCTTTACTCTGCTGGT 1492
 DB 183 GCTGGAAGCAAAATATCTGTTGGACATGATGAGATCATCTGCTTTACTCTGCTGGT 124
 QY 1493 CTGTACCGAGTTGTCATGGATCGATGTTCTTCATCCAAAGTTCAATATAGTCTCTCT 1552
 DB 123 CTGTACCGAGTTGTCATGGATCGATGTTCTTCATCCAAAGTTCAATATAGTCTCTCT 64
 QY 1553 GGAGCTGACATGTCATATATCTTTCCCATACATCCAGAGGCCAGCGACTCACTCTCTT 1612
 DB 63 GGAGCTGACATGTCATATATCTTTCCCATACATCCAGAGGCCAGCGACTCACTCTCTT 4
 QY 1613 CAT 1615
 DB 3 CAT 1

RESULT 7

ADC08843/c

ID ADC08843 standard; DNA; 258 BP.

XX

AC ADC08843;

XX

XX 18-DEC-2003 (first entry)

DT

DE

XX Corn DNA sequence Seq ID1148 related to grain filling.

XX

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;

KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;

KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;

KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;

KW gene; ds; plant.

XX

OS Zea mays.

XX

XX WO2003000905-A2.

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XX 03-JAN-2003.

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XX 21-JUN-2002; 2002WO-IB002450.

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XX 22-JUN-2001; 2001US-0300112P.

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XX 26-SEP-2001; 2001US-0325277P.

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XX 20-DEC-2001; 2001US-0342327P.

XX

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX

XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;

PI Glazebrook J, Katagiri F, Krepis J, Provart N, Ricke D;

XX

XX WPI; 2003-229341/22.

XX

XX New plant genes encoding polypeptides having an activity involved in or

PT associated with the synthesis, metabolism or degradation of carbohydrates

PT in the plant grain useful in generating plants having improved

PT nutritional properties.

XX

XX Disclosure; SEQ ID NO 1148; 130pp; English.

XX

XX This invention, in the area of plant biotechnology, relates to novel

CC polynucleotides comprising a nucleotide sequence encoding a protein which

CC is involved in or associated with the synthesis, metabolism or

CC degradation of carbohydrates in the plant grain and the expression of

CC which is up-regulated during grain filling. The plant is selected from

CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,

CC sugarbeet, wheat, and rice. The invention may be useful for the

CC improvement of protein, oil, starch, fibre and moisture content of the

CC cereal grains. In addition, carbohydrate levels may be modified to a more

CC desirable level using the present invention. The present sequence is a

CC DNA sequence from corn which showed homology to rice "grain filling"

CC genes of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at ftp.wipo.int/pub/publishedoct_sequences.

XX

XX Sequence 258 BP; 51 A; 87 C; 75 G; 45 T; 0 U; 0 Other;

XX

XX Query Match

XX Best Local Similarity 7.0%; Score 191; DB 9; Length 258;

XX

XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX 167 GCGAGGAGCCCTTCTTCGAGCTTCCTCGCGGAGGAGGATGCTGCGCGG 226

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XX 258 GCGAGGAGCCCTTCTTCGAGCTTCCTCGCGGAGGAGGATGCTGCGCGG 199

XX

XX 227 TTCGTGGCCATCGCGTGGCGCGCGCGGAGTTGGAGTACGTCGCGTCAAGTT 286

XX

XX 198 TTCGTGGCCATCGCGTGGCGCGCGCGGAGTTGGAGTACGTCGCGTCAAGTT 139

QY 287 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGAGTAGTACCTCCGCTTCAAGGAGGAGCTT 346

DB 138 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGAGTAGTACCTCCGCTTCAAGGAGGAGCTT 79

QY 347 GTCGACGCGCCA 357

DB 78 GTCGACGCGCCA 68

RESULT 8

ADA58359

ID ADA58359 standard; cDNA; 285 BP.

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AC ADA58359;

XX

DT 20-NOV-2003 (first entry)

XX

XX Maize sucrose synthase EST #3.

XX

KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;

KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;

KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;

KW phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;

KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;

KW invertase; sucrose synthase; hexokinase; fructokinase;

KW nucleoside diphosphate kinase-kinase; NDP;

KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;

KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX

OS Zea mays.

XX

XX US2003135870-A1.

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XX 17-JUL-2003.

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XX 26-JAN-1999; 99US-00237183.

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XX 24-NOV-1997; 97US-0067000P.

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XX 09-DEC-1997; 97US-0069472P.

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XX 27-JAN-1998; 98US-0072888P.

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XX 10-FEB-1998; 98US-0074201P.

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XX 10-FEB-1998; 98US-0074280P.

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XX 10-FEB-1998; 98US-0074282P.

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XX 12-FEB-1998; 98US-0074565P.

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XX 19-FEB-1998; 98US-0074789P.

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XX 19-FEB-1998; 98US-0075459P.

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XX 19-FEB-1998; 98US-0075460P.

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XX 19-FEB-1998; 98US-0075461P.

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XX 19-FEB-1998; 98US-0075462P.

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XX 19-FEB-1998; 98US-0075463P.

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XX 06-MAR-1998; 98US-0076912P.

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XX 09-MAR-1998; 98US-0077229P.

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XX 09-MAR-1998; 98US-0077230P.

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XX 09-MAR-1998; 98US-0077231P.

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XX 18-MAR-1998; 98US-0078368P.

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XX 27-APR-1998; 98US-0080844P.

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XX 29-APR-1998; 98US-0083067P.

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XX 29-APR-1998; 98US-0083386P.

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XX 29-APR-1998; 98US-0083387P.

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XX 29-APR-1998; 98US-0083388P.

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XX 29-APR-1998; 98US-0083389P.

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XX 29-APR-1998; 98US-0083390P.

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XX 13-MAY-1998; 98US-0085222P.

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XX 13-MAY-1998; 98US-0085223P.

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XX 13-MAY-1998; 98US-0085224P.

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XX 21-MAY-1998; 98US-0086183P.

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XX 21-MAY-1998; 98US-0086184P.

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XX 21-MAY-1998; 98US-0086185P.

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XX 21-MAY-1998; 98US-0086186P.

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 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
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 PR 13-MAY-1998; 98US-0085223P.
 PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089810P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0098667P.
 PR 09-SEP-1998; 98US-0099670P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101344P.
 PR 21-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.
 XX (CHEI/) CHEIKH N.
 PA (FISH/) FISHER D K.
 PA (LIU/) LIU J.
 XX Cheikh N, Fisher DK, Liu J;
 XX WPI; 2003-688722/65.
 XX
 PT New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and
 PT analysis, plant breeding, or preparation of constructs for plant gene
 PT expression.
 XX
 PS Claim 2; Page; 117pp; English.

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 CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC transformed plant having a nucleic acid molecule. Also disclosed as new
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
 XX
 SQ Sequence 297 BP; 92 A; 51 C; 65 G; 89 T; 0 U; 0 Other;
 Query Match 5.8%; Score 158; DB 8; Length 297;
 Best Local Similarity 99.2%; Pred. No. 2.3e-52;
 Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1102 TAAGAAATGGATATCAAGATTGATGTGGCCATATCTGGAACATTGCTGAGGATGC 1161
 DB 2 TAAGAAATGGATATCAAGATTGATGTGGCCATATCTGGAACATTGCTGAGGATGC 61
 QY 1162 TGCTGGTGAATTCGCTGCTGAATTAAGGTAATCCAGACTTCAATATGGAACTACAG 1221
 DB 62 TGCTGGTGAATTCGCTGCTGAATTAAGGTAATCCAGACTTCAATATGGAACTACAG 121
 QY 1222 TGATGAAATCTTGTGGCGTCATTGCTATCTTCAAGATGGGAATTACCCAGTGCACAT 1281
 DB 122 TGATGAAATCTTGTGGCGTCATTGCTATCTTCAAGATGGGAATTACCCAGTGCACAT 181
 QY 1282 TGCTCATGCTCTGAAAGAACTAAGTATCCAGATTCAGACATATTTGGAGAAATTCGA 1341
 DB 182 TGCTCATGCTCTGAAAGAACTAAGTATCCAGATTCAGACATATTTGGAGAAATTCGA 241
 QY 1342 TGAGAGTACCAATTCCTCT 1361
 DB 242 TGAGAGTACCAATTCCTCT 261
 RESULT 10
 ADA56373
 ID ADA56373 standard; cDNA; 150 BP.
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 AC ADA58373;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Maize sucrose synthase EST #17.
 XX
 XX Plant; sg; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;

121 GTTCAATCGAAATTGATTATGACCGG 150

Db
RESULT 11
ADA58864
ADA58864 standard; cDNA; 411 bp.
AC
AC ADA58864;
DT
DT 20-NOV-2003 (first entry)
DE
DE Maize sucrose synthase EST #508.
KW
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW Glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
XX Zea mays.
XX
XX US2003:35870-A1.
PD
PD 17-JUL-2003.
XX
XX 26-JAN-1999; 99US-00237183.
XX
XX 24-NOV-1997; 97US-0067000P.
PR
PR 09-DEC-1997; 97US-0069472P.
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PR 27-JAN-1998; 98US-0072888P.
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PR 10-FEB-1998; 98US-0074282P.
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PR 12-FEB-1998; 98US-0074555P.
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PR 12-FEB-1998; 98US-0074566P.
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PR 12-FEB-1998; 98US-0074567P.
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PR 19-FEB-1998; 98US-0074789P.
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PR 19-FEB-1998; 98US-0075461P.
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PR 06-MAR-1998; 98US-0076912P.
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PR 09-MAR-1998; 98US-0077229P.
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PR
PR 18-MAR-1998; 98US-0078368P.
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PR 07-APR-1998; 98US-0080044P.
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PR 27-APR-1998; 98US-0083067P.
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PR 29-APR-1998; 98US-0083386P.
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PR
PR 21-MAY-1998; 98US-0086183P.
PR
PR 21-MAY-1998; 98US-0086184P.
PR
PR 21-MAY-1998; 98US-0086185P.
PR
PR 21-MAY-1998; 98US-0086186P.
PR
PR 21-MAY-1998; 98US-0086187P.
PR
PR 21-MAY-1998; 98US-0086188P.
PR
PR 01-JUN-1998; 98US-0087422P.
PR
PR 16-JUN-1998; 98US-0089524P.
PR
PR 18-JUN-1998; 98US-0089793P.

PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
PR 09-SEP-1998; 98US-0099697P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 18-NOV-1998; 98US-0104128P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX
XX (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIUJ/) LIU J.

Cheikh N, Fisher DK, Liu J;

WPI; 2003-688722/65.

New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression.

Claim 2; Page: 117pp; English.

The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from: triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose 1,6-phosphate, fructose 6-phosphate 2-kinase, phosphoglucosyltransferase, vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent fructose-6-phosphate phosphotransferase, invertase, sucrose synthase, hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase, glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine diphosphate (UDP)-glucose pyrophosphorylase. Also included are a substantially purified maize or soybean enzyme (or its fragment) and a transformed plant having a nucleic acid molecule. Also disclosed as new are purified antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway enzyme in a plant cell or plant tissue, determining a mutation in a plant whose presence is predictive of a mutation affecting the level or pattern of a plant sucrose pathway enzyme, producing a plant containing an overexpressed or reduced level of plant sucrose pathway enzyme, reducing expression of a plant sucrose pathway enzyme in a plant and determining an association between a polymorphism and a plant trait. The maize or soybean enzymes and nucleic acid molecules are useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression and transgenic plants. The nucleic acid molecules are also useful as markers or probes. The present sequence

CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX SQ Sequence 411 BP; 99 A; 109 C; 113 G; 88 T; 0 U; 2 Other;

Query Match 5.2%; Score 143; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. NO. 1.9e-46;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1739 GGGCTGGTCCAGCTTTTCTAAGTGGCTTAAGCTGAGGGAGCTGTAACCTTGTGCTC 1798

DB 88 GGGCTGGTCCAGCTTTTCTAAGTGGCTTAAGCTGAGGGAGCTGTAACCTTGTGCTC 147

QY 1799 GTTGGCGGGTACAATGATGTCACCAAGTCCAGGACAGGAGAGATCCGGAGATAGAG 1858

DB 148 GTTGGCGGGTACAATGATGTCACCAAGTCCAGGACAGGAGAGATCCGGAGATAGAG 207

QY 1859 AAGATGCATGAACCTCATCAAGAC 1881

DB 208 AAGATGCATGAACCTCATCAAGAC 230

RESULT 12

ADA58374

ID ADA58374 standard; cDNA; 255 BP.

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

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XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

XX AC ADA58374;

CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucosomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucosomase and uridine
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
XX
SQ Sequence 255 BP; 63 A; 62 C; 67 G; 63 T; 0 U; 0 Other;

Query Match 4.9%; Score 134; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 7e-43;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 564 ATGATAGAAATACAAAGCTTGGGGAGGCTTCAGTCTGTCTGACCAAAAGCTCAGGAGCACT 623
Db |||||||
110 ATGATAGAAATACAAAGCTTGGGGAGGCTTCAGTCTGTCTGACCAAAAGCTCAGGAGCACT 169

QY 624 TGTCAAAGCTCCCTGCTGACACACATCTCACAAATTTGCTTATAAATTTCAAGAGTGGG 683
Db |||||||
170 TGTCAAAGCTCCCTGCTGACACACATCTCACAAATTTGCTTATAAATTTCAAGAGTGGG 229

QY 684 GCCTGGAGAAAGGT 697
Db |||||||
230 GCCTGGAGAAAGGT 243

RESULT 13
ADA58370
ID ADA58370 standard; cDNA; 181 BP.
AC ADA58370;
XX
DT 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #14.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucosomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucosomase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-A1.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 99US-00237183.
XX
XX 24-NOV-1997; 97US-0067000P.
PR

PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 12-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083386P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083389P.
PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
PR 09-SEP-1998; 98US-0099672P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210237.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.

Db 170 TGTCAGAGCTCCCTGTCGACACACCACTACCAATTTGCTTATAAATTTCCAGAGTGGG 229
 QY 684 GC 685
 Db 230 GC 231
 RESULT 15
 ADA58369
 ID ADA58369 standard; cDNA; 310 BP.
 XX AC ADA58369;
 XX DT 20-NOV-2003 (first entry)
 XX DE Maize sucrose synthase EST #13.
 XX KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
 KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; UDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.
 XX Zea mays.
 CS US2003135870-A1.
 PN 17-JUL-2003.
 XX PD 26-JAN-1999; 99US-00237183.
 XX PF 24-NOV-1997; 97US-0067000P.
 XX PR 09-DEC-1997; 97US-0069472P.
 PR 27-JAN-1998; 98US-0072888P.
 PR 10-FEB-1998; 98US-0074201P.
 PR 10-FEB-1998; 98US-0074280P.
 PR 10-FEB-1998; 98US-0074281P.
 PR 10-FEB-1998; 98US-0074282P.
 PR 12-FEB-1998; 98US-0074565P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
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 PR 19-FEB-1998; 98US-0075459P.
 PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
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 PR 06-MAR-1998; 98US-0076912P.
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 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.

PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
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 PR 18-JUN-1998; 98US-0089810P.
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 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
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 PR 09-SEP-1998; 98US-0099670P.
 PR 09-SEP-1998; 98US-0099697P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
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 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
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 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.
 XX (CHEI/) CHEIKH N.
 PA (FISH/) FISHER D K.
 PA (LIU/) LIU J.
 XX Cheikh N, Fisher DK, Liu J;
 WPI; 2003-688722/65.
 XX New maize or soybean enzymes and nucleic acid molecules associated with
 the sucrose pathway, useful for genome mapping, Gene identification and
 analysis, plant breeding, or preparation of constructs for plant gene
 expression.
 XX Claim 2; Page; 117pp; English.
 XX The invention relates to a substantially purified nucleic acid molecule
 (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
 or its fragment, associated with the sucrose pathway selected from:
 triose phosphate isomerase, fructose 1, 6-bisphosphate aldolase, fructose
 1, 6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
 vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
 diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 substantially purified maize or soybean enzyme (or its fragment) and a
 transformed plant having a nucleic acid molecule. Also disclosed as new
 are purified antibodies capable of specifically binding to the maize or
 soybean enzyme, determining a level or pattern of a plant sucrose pathway
 enzyme in a plant cell or plant tissue, determining a mutation in a plant
 whose presence is predictive of a mutation affecting the level or pattern
 of a plant sucrose pathway enzyme, producing a plant containing an
 overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 expression of a plant sucrose pathway enzyme in a plant and determining
 an association between a polymorphism and a plant trait. The maize or
 soybean enzymes and nucleic acid molecules are useful for genome mapping,

CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.

XX
 SQ Sequence 310 BP; 89 A; 62 C; 64 G; 94 T; 3 U; 1 Other;

Query Match 4.2%; Score 114; DB 8; Length 310;
 Best Local Similarity 99.4%; Pred. No. 5.2e-35;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1364	CAGTTCACCTGCTGATATTAATGCTATGCAACAAATGCTGATTTATCATCACGACATAC	1423
DB	146	CAGTTCACCTGCTGATATTAATGCTATGCAACAAATGCTGATTTATCATCACGACATAC	205
QY	1424	CAAGAAATGCTGGAAGCAAAATACCTGTGGACAGTATGAGAGTCATCTGCCCTTTACT	1483
DB	206	CAAGAAATGCTGGAAGCAAAATACCTGTGGACAGTATGAGAGTCATCTGCCCTTTACT	265
QY	1484	CTGCCCTGCTGTACCGAGTGTCCATGGGATCGATGCTTCGAT	1528
DB	266	CTGCCCTGCTGTACCGAGTGTCCATGGGATCGATGCTTCGAT	310

Search completed: May 26, 2004, 02:50:33
 Job time : 691.979 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 01:50:38 ; Search time 4543.9 Seconds
(without alignments)

17987.372 Million cell updates/sec

Title: US-10-080-114A-1

Perfect score: 2737

Sequence: 1 gtcacccagcggtccggc.....aaaaaaaaaagggcgccgc 2737

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 50

Total number of hits satisfying chosen parameters: 84

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmd.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_esti.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estcom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pdg.*

27: em_gss_vrt.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1693	61.9	2705	11	AY104856
2	464	17.0	902	13	BQ619510
3	351	12.8	411	12	BM500505
4	329	12.0	722	28	BZ322655

C	5	329	12.0	773	28	BZ316142
C	6	329	12.0	794	28	CC394967
C	7	329	12.0	813	29	CG069438
C	8	329	12.0	840	29	CC667244
	9	329	12.0	982	29	CG069436
	10	321	11.7	938	13	BQ619406
	11	321	11.7	1005	13	BQ619258
	12	317	11.6	662	28	BZ322987
	13	313	11.4	313	14	CD984711
	14	313	11.4	313	14	CD984732
	15	312	11.4	316	14	CD984116
	16	288	10.5	313	14	CD985046
	17	287	10.5	435	12	BM500263
	18	224	8.2	573	14	CF630867
	19	224	8.2	645	28	BZ316481
C	20	217	7.9	731	29	CC733515
C	21	207	7.6	546	10	AW324745
	22	200	7.3	690	14	CD442316
	23	193	7.1	329	14	CD984266
C	24	158	5.8	315	29	CG275613
C	25	158	5.8	338	29	CG221855
	26	158	5.8	499	10	BF728272
	27	158	5.8	593	13	BUL02935
C	29	158	5.8	593	13	CA097247
	30	158	5.8	648	29	CG377054
	31	158	5.8	700	14	CA195492
	32	157	5.7	797	29	CC628483
C	33	156	5.7	908	29	CC628491
C	34	156	5.7	272	29	CG317557
C	35	156	5.7	445	29	CG659484
C	36	156	5.7	746	29	CG442293
C	37	154	5.6	182	28	BZ641724
C	38	154	5.6	197	28	BZ543980
C	39	148	5.4	332	9	AI973432
	40	147	5.4	188	28	BZ641703
	41	146	5.3	804	28	BZ723706
C	42	144	5.3	324	14	CF637987
C	43	140	5.1	637	29	CC609870
C	44	136	5.0	815	29	CG004867
	45	128	4.7	504	29	CG275601

ALIGNMENTS

RESULT 1	AY104856	2705 bp	mrna	linear	HTC 16-OCT-2002
LOCUS	AY104856	2705 bp	mrna	linear	HTC 16-OCT-2002
DEFINITION	Zea mays PC0079420	mrna sequence.			
ACCESSION	AY104856				
VERSION	AY104856.1	GI:21207934			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.				
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of				
JOURNAL	Overgo Probes				
REFERENCE	Unpublished (2002)				
AUTHORS	1 (bases 1 to 2705)				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of				
COMMENT	Missouri, Columbia, MO 65211, USA				
	If you are interested in getting corresponding physical clones,				
	these are publicly available from ZmDB and may be found by BLAST				
	searching at MSL, maizemap.org ; ZmDB, www.zmdb.iastate.edu ; TIGR,				
	www.tigr.org ; or NCBI, www.ncbi.nlm.nih.gov . When the source of the				


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QY 1878 AGACCCAGCACTGTTCCGGCAGTTCCCGTGGTCTCTGCCCAGACAAACAGAGCCCGTA 1937
Db 1861 AGACCCAGCACTGTTCCGGCAGTTCCCGTGGTCTCTGCCCAGACAAACAGAGCCCGTA 1920
QY 1938 ACGGCGAGCTCTATCGCTACATCGCTGATACCCATGCTTTCGTCACAGCCGCGCTTGT 1997
Db 1921 ACGGCGAGCTCTATCGCTACATCGCTGATACCCATGCTTTCGTCACAGCCGCGCTTGT 1980
QY 1998 ATGAAGCGTTCGGTCTCAGCTCGTTCAGCCGTCAGCCATGACCTGTGGCTTCCTACTTCGCGA 2057
Db 1981 ATGAAGCGTTCGGTCTCAGCTCGTTCAGCCGTCAGCCATGACCTGTGGCTTCCTACTTCGCGA 2040
QY 2058 CCGTCCAGAGGTCAGCTGATGATCATAGAGTGGCTCTCGGCTCCACATTTGACC 2117
Db 2041 CCGTCCAGAGGTCAGCTGATGATCATAGAGTGGCTCTCGGCTCCACATTTGACC 2100
QY 2118 CGTACACACCCCAAGAGGCTGTTAATCTCATGSCCGACTTCTTCGACCGGTGCAAGCAAG 2177
Db 2101 CGTACACACCCCAAGAGGCTGTTAATCTCATGSCCGACTTCTTCGACCGGTGCAAGCAAG 2160
QY 2178 ACCGAGATCACTGGGTGAATATATCTGGAGCGGGCTCGAGCGCATATACGAGAATACA 2237
Db 2161 ACCGAGATCACTGGGTGAATATATCTGGAGCGGGCTCGAGCGCATATACGAGAATACA 2220
QY 2238 CATGAGAGTATCTCAGAGAGGTTGATGACACTGGCCGGGCTCTACGGTCTTCGAGCT 2297
Db 2221 CATGAGAGTATCTCAGAGAGGTTGATGACACTGGCCGGGCTCTACGGTCTTCGAGCT 2280
QY 2298 AGCTGCGAGCTCGAGAGGCTGGAGACGAGCGCTACCTTCGAGATGTTCTACATCTGA 2357
Db 2281 AGCTGCGAGCTCGAGAGGCTGGAGACGAGCGCTACCTTCGAGATGTTCTACATCTGA 2340
QY 2358 AGTTCGCGAGCTGCGAAGACGCTGCCGCTTGCATTTGCAATGACCAACCGCGAGTCTTGCGC 2417
Db 2341 AGTTCGCGAGCTGCGAAGACGCTGCCGCTTGCATTTGCAATGACCAACCGCGAGTCTTGCGC 2400
QY 2418 AACTCGACTGCTGAGCACTTGGTCAAGACATGACCTGAGGACCTTCAGTAATTTAG 2477
Db 2401 AACTCGACTGCTGAGCACTTGGTCAAGACATGACCTGAGGACCTTCAGTAATTTAG 2460
QY 2478 GCGCGCAGCGGTAGCCAAATAAATGTGCCGAGCTGAACTGGTTTTT 2526
Db 2461 GCGCGCAGCGGTAGCCAAATAAATGTGCCGAGCTGAACTGGTTTTT 2509

RESULT 2
BQ619510/c
LOCUS BQ619510 902 bp mRNA linear EST 06-SEP-2002
DEFINITION RESEQ1B02_SK.ab1 Salt stressed Zea mays roots cDNA library Zea mays
CDNA clone RESEQ1B02_SK.ab1 similar to sucrose synthase [Zea mays],
mRNA sequence.
ACCESSION BQ619510
VERSION BQ619510.1 GI:21621504
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 902)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. .902
/organism="Zea mays"
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/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="RESEQ1B02_SK.ab1"
/tissue_type="Roots"
/dev_stage="2 weeks old"
/clone_lib="Salt stressed Zea mays roots cDNA library"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150 mM NaCl"
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ORIGIN

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Query Match 17.0%; Score 464; DB 13; Length 902;
Best Local Similarity 100.0%; Pred. No. 3e-84;
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 CTAGAGAAATCTTGGGGAGGATCCCATCAATTTTAAACGTTGTGTGGTATCCCTCAT 835
Db 551 CTAGAGAAATCTTGGGGAGGATCCCATCAATTTTAAACGTTGTGTGGTATCCCTCAT 492
QY 836 GGATACCTTTGGTCAAGCTAATGTTAGGCTTCCGACACACAGGAGCAGATCGTCTAT 895
Db 491 GGATACCTTTGGTCAAGCTAATGTTAGGCTTCCGACACACAGGAGCAGATCGTCTAT 432
QY 896 ATACTGGACCAAGTCCGTCACCTAGAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGG 955
Db 431 ATACTGGACCAAGTCCGTCACCTAGAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGG 372
QY 956 CTTGATGTTTCCCAAGATTCATTTGTTACTCGGCTGATACAGATGCAAAAGGAACA 1015
Db 371 CTTGATGTTTCCCAAGATTCATTTGTTACTCGGCTGATACAGATGCAAAAGGAACA 312
QY 1016 TCATGCAATCAGCGCTTCGAGAAATAGTGGAAACACAGCATCTTACATATTACGAGTT 1075
Db 311 TCATGCAATCAGCGCTTCGAGAAATAGTGGAAACACAGCATCTTACATATTACGAGTT 252
QY 1076 CCCTTCAGAAATGAAATGGGATACCTTAAAGATGGATATCAAGATTTGATGTGGCCA 1135
Db 251 CCCTTCAGAAATGAAATGGGATACCTTAAAGATGGATATCAAGATTTGATGTGGCCA 192
QY 1136 TATCTGGAACATTTCTGAGGATGCTGCTGGTGAATTCCTGCTGAATTAACAGGTA 1195
Db 191 TATCTGGAACATTTCTGAGGATGCTGCTGGTGAATTCCTGCTGAATTAACAGGTA 132
QY 1196 CCAGACTTCATATTCGAAACTACAGTATGGAATCTTGTGGC 1239
Db 131 CCAGACTTCATATTCGAAACTACAGTATGGAATCTTGTGGC 89
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RESULT 3

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BQ619510
LOCUS BQ619510 411 bp mRNA linear EST 14-FEB-2002
DEFINITION Pioneer AF-1 array Zea mays cDNA, mRNA sequence.
ACCESSION BQ619510
VERSION BQ619510.1 GI:18659754
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 411)
Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
Jung, R.
Maize opaque endosperm mutations create extensive changes in
patterns of gene expression
Unpublished (2002)
Contact: Jung R
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa069E23"
/clone_lib="ZM_0.6_1.0_KB"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

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ORIGIN

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Query Match      12.0%; Score 329; DB 29; Length 813;
Best Local Similarity 100.0%; Pred. No. 3.5e-57;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GCGGAGACGCGCCGCTTGCAGTACCAACCGAGTGTGCGCACTGGCGTGG 2430
      |||
Db 730 GCGGAGACGCGCGCTTGCAGTACCAACCGAGTGTGCGCACTGGCGTGG 671

QY 2431 TAGCACTTGGTCAAGACTGAAACCTGAAGGACCTTCAGTAATTTAGGCGCGGACGCG 2490
      |||
Db 670 TAGCACTTGGTCAAGACTGAAACCTGAAGGACCTTCAGTAATTTAGGCGCGGACGCG 611

QY 2491 TAGCCAATAAATGTGCCGAGCTGAACCTGGTTTTTATATGTACATAATGGCAGTATA 2550
      |||
Db 610 TAGCCAATAAATGTGCCGAGCTGAACCTGGTTTTTATATGTACATAATGGCAGTATA 551

QY 2551 ACAAAATTAATGAGGACGCGGTGCGAGTGTGCGTGTGCTTACTGTATTAT 2610
      |||
Db 550 ACAAAATTAATGAGGACGCGGTGCGAGTGTGCGTGTGCTTACTGTATTAT 491

QY 2611 GTCAAGCTGTGCGCTGCATTTCTTTGTGCGAAGCGGACGCTGTGTAAGTGTGAT 2670
      |||
Db 490 GTCAAGCTGTGCGCTGCATTTCTTTGTGCGAAGCGGACGCTGTGTAAGTGTGAT 431

QY 2671 AAATACATCATATTCCTGTGACCTGTGAA 2699
      |||
Db 430 AAATACATCATATTCCTGTGACCTGTGAA 402

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RESULT 8
CC667244
LOCUS
DEFINITION
  CC667244 OGWC96TH ZM 0.7 1.5 KB Zea mays genomic clone ZMBMa0534023,
  genomic survey sequence.
ACCESSION
  CC667244
VERSION
  CC667244.1 GI:32071336
KEYWORDS
  GSS.
SOURCE
  Zea mays
  Zea mays
  Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 840)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
  Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  Consortium for Maize Genomics
  Unpublished (2002)
  Other_GSSs: OGWC96TV
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TR
  Class: sheared ends.
  Location/Qualifiers
    1..840
    /organism="Zea mays"
    /mol_type="genomic DNA"
    /strain="B73"
    /db_xref="taxon:4577"

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FEATURES

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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

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/notes="Vector: pBCK-7; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

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Query Match      12.0%; Score 329; DB 29; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.4e-57;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GCGGAGACGCGCGCTTGCAGTACCAACCGAGTGTGCGCACTGGCGTGG 2430
      |||
Db 423 GCGGAGACGCGCGCTTGCAGTACCAACCGAGTGTGCGCACTGGCGTGG 482

QY 2431 TAGCACTTGGTCAAGACTGAAACCTGAAGGACCTTCAGTAATTTAGGCGCGGACGCG 2490
      |||
Db 483 TAGCACTTGGTCAAGACTGAAACCTGAAGGACCTTCAGTAATTTAGGCGCGGACGCG 542

QY 2491 TAGCCAATAAATGTGCCGAGCTGAACCTGGTTTTTATATGTACATAATGGCAGTATA 2550
      |||
Db 543 TAGCCAATAAATGTGCCGAGCTGAACCTGGTTTTTATATGTACATAATGGCAGTATA 602

QY 2551 ACAAAATTAATGAGGACGCGGTGCGAGTGTGCGTGTGCTTACTGTATTAT 2610
      |||
Db 603 ACAAAATTAATGAGGACGCGGTGCGAGTGTGCGTGTGCTTACTGTATTAT 662

QY 2611 GTCAAGCTGTGCGCTGCATTTCTTTGTGCGAAGCGGACGCTGTGTAAGTGTGAT 2670
      |||
Db 663 GTCAAGCTGTGCGCTGCATTTCTTTGTGCGAAGCGGACGCTGTGTAAGTGTGAT 722

QY 2671 AAATACATCATATTCCTGTGACCTGTGAA 2699
      |||
Db 723 AAATACATCATATTCCTGTGACCTGTGAA 751

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RESULT 9
CG069436
LOCUS
DEFINITION
  CG069436 PUFKE36TB ZM 0.6 1.0 KB Zea mays genomic clone ZMBMa069E23,
  genomic survey sequence.
ACCESSION
  CG069436
VERSION
  CG069436.1 GI:33941616
KEYWORDS
  GSS.
SOURCE
  Zea mays
  Zea mays
  Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 982)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other_GSSs: PUFKE36TD
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TR
  Class: sheared ends.
  Location/Qualifiers
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    /organism="Zea mays"
    /mol_type="genomic DNA"
    /strain="B73"
    /db_xref="taxon:4577"
    /clone="ZMBMa069E23"
    /clone_lib="ZM_0.6_1.0_KB"
    /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
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FEATURES

source

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1..982
/organism="Zea mays"
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cot selected genomic DNA library"

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ORIGIN
Query Match      12.0%; Score 329; DB 29; Length 982;
Best Local Similarity 100.0%; Pred. No. 2.9e-57;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2371 GCGAAGACCGTGGCGGTTCGAATTGACCAACCGCAGTAGCTTCGCGCAACTGCGACTGCG 2430
Db 312 GCGAAGACCGTGGCGGTTCGAATTGACCAACCGCAGTAGCTTCGCGCAACTGCGACTGCG 371
Qy 2431 TAGCACTTGTGACAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 2490
Db 372 TAGCACTTGTGACAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 431
Qy 2491 TAGCACTTGTGACAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 2550
Db 432 TAGCACTTGTGACAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 491
Qy 2551 ACAAATTTACTGAAGGAGGTGGGTTCGAGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTT 2610
Db 492 ACAAATTTACTGAAGGAGGTGGGTTCGAGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTT 551
Qy 2611 GTCAGCTGTCGGTGCATTTCTTTGTCGCAAGCCGCGAGCACTGTCGAAGTCTGAT 2670
Db 552 GTCAGCTGTCGGTGCATTTCTTTGTCGCAAGCCGCGAGCACTGTCGAAGTCTGAT 611
Qy 2671 AATACATCATATCTCTTGACCTGTGAA 2699
Db 612 AATACATCATATCTCTTGACCTGTGAA 640

RESULT 10
BO619406
LOCUS BO619406 938 bp mRNA linear EST 06-SEP-2002
DEFINITION RNOSE07D02_SK.abl Salt stressed Zea mays roots cDNA library [Zea mays], mRNA sequence.
ACCESSION BO619406
VERSION BO619406.1 GI:21621400
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 938)
AUTHORS Wang,H. and Bohnert,H.J.
TITLE Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
JOURNAL Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
COMMENT clade; Panicoideae; Andropogoneae; Zea.

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                        /mol_type="mRNA"
                        /cultivar="B73"
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                        /tissue_type="Roots"
                        /dev_stage="2 weeks old"
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Query Match      11.7%; Score 321; DB 13; Length 938;
Best Local Similarity 100.0%; Pred. No. 1.2e-55;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2198 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 2257
Db 418 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 477
Qy 2258 AGGTTGATGACATCGCGGGGTCTACGGTTTCTGGAAGTACGTTCGAAGCTCGAGAGG 2317
Db 418 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 477
Qy 2258 AGGTTGATGACATCGCGGGGTCTACGGTTTCTGGAAGTACGTTCGAAGCTCGAGAGG 2317
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Qy 2198 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 2257
Db 418 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 477
Qy 2258 AGGTTGATGACATCGCGGGGTCTACGGTTTCTGGAAGTACGTTCGAAGCTCGAGAGG 2317
Db 478 AGGTTGATGACATCGCGGGGTCTACGGTTTCTGGAAGTACGTTCGAAGCTCGAGAGG 537
Qy 2318 CTGGAGACGAGCGCTACCTTGAGATGTTCTACATCTGGAAGTTCGCGAGCTGCGGAAG 2377
Db 538 CTGGAGACGAGCGCTACCTTGAGATGTTCTACATCTGGAAGTTCGCGAGCTGCGGAAG 597
Qy 2378 ACCGTGCGCGTTGCAATTGACCAACCGCAGTAGCTTCGCGCAACTCGGACTGCGTAGCACT 2437
Db 598 ACCGTGCGCGTTGCAATTGACCAACCGCAGTAGCTTCGCGCAACTCGGACTGCGTAGCACT 657
Qy 2438 TGGTACAAAGCTGAAACCTGGAAGACCTTCAGTAAATTTAGGCGCGGCGAGACCGGTAGCCAA 2497
Db 658 TGGTACAAAGCTGAAACCTGGAAGACCTTCAGTAAATTTAGGCGCGGCGAGACCGGTAGCCAA 717
Qy 2498 TAAATGTGCGGAGCTGAAC 2518
Db 718 TAAATGTGCGGAGCTGAAC 738

RESULT 11
BO619258
LOCUS BO619258 1005 bp mRNA linear EST 06-SEP-2002
DEFINITION RNOSE05F01_SK.abl Salt stressed Zea mays roots cDNA library [Zea mays], mRNA sequence.
ACCESSION BO619258
VERSION BO619258.1 GI:21621252
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 1005)
AUTHORS Wang,H. and Bohnert,H.J.
TITLE Genomics of plant stress tolerance
JOURNAL Unpublished (2002)
COMMENT Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.

FEATURES
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                        /organism="Zea mays"
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                        /dev_stage="2 weeks old"
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ORIGIN
Query Match      11.7%; Score 321; DB 13; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.2e-55;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2198 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 2257
Db 418 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAATATATCTACTCAGAG 477
Qy 2258 AGGTTGATGACATCGCGGGGTCTACGGTTTCTGGAAGTACGTTCGAAGCTCGAGAGG 2317
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Db      121  GGTTCATCGAAATTTGATTATGACCCGAGCAAAACGATGAACACATTTGGGCACTG 180
Qy      1676  GATGACCGGTCAAGCCCACTCTCTCTCCATGGCAGACTCGACAGGCTGAAGAACATA 1735
Db      181  GATGACCGGTCAAGCCCACTCTCTCTCCATGGCAGACTCGACAGGCTGAAGAACATA 240
Qy      1736  ACAGGGCTGGTGGAGCTTTTGTAACTGGCTAACTGAGGAGCTGGTAAACCTTTGTC 1795
Db      241  ACAGGGCTGGTGGAGCTTTTGTAACTGGCTAACTGAGGAGCTGGTAAACCTTTGTC 300
Qy      1796  GTCGTTGCCGGGT 1808
Db      301  GTCGTTGCCGGGT 313

RESULT 14
LOCUS   CD984732
DEFINITION QAM24h06.yg QAM Zea mays cDNA clone QAM24h06, mRNA linear EST 16-JUL-2003
ACCESSION CD984732
VERSION   CD984732.1 GI:32845051
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 313)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.3e-53;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1496  TACCGAGTTGTCATGGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCTGGA 1555
Db      1 TACCGAGTTGTCATGGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCTGGA 60
Qy      1556  GCTGACATGTCATATACCTTCCATACCGAGAGCCCAAGCGACTCACCTCTCTTCAT 1615
Db      61  GCTGACATGTCATATACCTTCCATACCGAGAGCCCAAGCGACTCACCTCTCTTCAT 120
Qy      1616  GGTTCATCGAAATTTGATTATGACCCGAGCAAAACGATGAACACATTTGGGCACTG 1675
Db      121  GGTTCATCGAAATTTGATTATGACCCGAGCAAAACGATGAACACATTTGGGCACTG 180
Qy      1676  GATGACCGGTCAAGCCCACTCTCTCTCCATGGCAGACTCGACAGGCTGAAGAACATA 1735
Db      181  GATGACCGGTCAAGCCCACTCTCTCTCCATGGCAGACTCGACAGGCTGAAGAACATA 240
Qy      1736  ACAGGGCTGGTGGAGCTTTTGTAACTGGCTAACTGAGGAGCTGGTAAACCTTTGTC 1795
Db      241  ACAGGGCTGGTGGAGCTTTTGTAACTGGCTAACTGAGGAGCTGGTAAACCTTTGTC 300

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Qy      1796  GTCGTTGCCGGGT 1808
Db      301  GTCGTTGCCGGGT 313

RESULT 15
LOCUS   CD984116
DEFINITION QAM17g10.yg QAM Zea mays cDNA clone QAM17g10, mRNA linear EST 16-JUL-2003
ACCESSION CD984116
VERSION   CD984116.1 GI:32844435
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 316)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
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Search completed: May 26, 2004, 09:17:58
Job time : 4550.9 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:35:47 ; Search time 7060.61 Seconds
(without alignments)
16924.423 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

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Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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14: gb_vi.*

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16: em_fun.*

17: em_hum.*

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19: em_mu.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1989	72.1	2837	8	AY124703	AY124703 Zea mays
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9	103	3.7	239	11	BV079812	BV079812 sc1180_p3
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ALIGNMENTS

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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

AY059416
Zea mays sucrose synthase mRNA, partial cds.
AY059416
AY059416.1 GI:16797784
Zea mays
Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2710)
Carlson, S.J., Chourey, P.S., Helentjaris, T. and Datta, R.
Gene expression studies on developing kernels of maize sucrose
synthase (Susy) mutants show evidence for a third Susy gene
Plant Mol. Biol. (2001) In press
2 (bases 1 to 2710)
Helentjaris, T.
Direct Submission
Submitted (10-OCT-2001) Agronomic Traits/T&T, Pioneer Hi-Bred,
7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA

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CDS

ORIGIN

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Matches 2561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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307 CACGAGCTCAGCGTCCGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTT 366
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Db CACTTGTCTCCTCAATCATGTTCCGCAACAGGAGTTGTTGGAGCCCTGTTGGATTTCCTC 509

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AUTHORS Holtgraeve, D.L., Scholz, A., Altmann, B. and Winter, H.
TITLE Complete coding sequence of a third sucrose synthase isoform in maize
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2837)
AUTHORS Holtgraeve, D.L., Scholz, A., Altmann, B. and Winter, H.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) Biology, University of Osnabrueck, Barbara
Strasse 11, Osnabrueck 49076, Germany
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QY 1867 GCGGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1926
Db 1987 GCGGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2046
QY 1927 TGGATCTCTGCCAGACAAACAGGGCCCGTAAACGGGAGCTCTATCGCTACATCGCTGAT 1986
Db 2047 TGGATCTCTGCCAGACAAACAGGGCCCGTAAACGGGAGCTCTATCGCTACATCGCTGAT 2106
QY 1987 ACCATGCTGCTTTCGTACAGCCGGCTTGTATGAAAGCGTTTGGTCTCACCGTCTGTGAG 2046
Db 2107 ACCATGCTGCTTTCGTACAGCCGGCTTGTATGAAAGCGTTTGGTCTCACCGTCTGTGAG 2166
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QY 2047 GCATGACCTGTGGGCTTCTTCTACTTTTCGAGAGCTCCATGGAGGTCCAGCTGAGATCATA 2106
Db 2167 GCATGACCTGTGGGCTTCTTCTACTTTTCGAGAGCTCCATGGAGGTCCAGCTGAGATCATA 2226
QY 2107 GAGCATGGGCTCTCGGGCTTCCACATTTGACCCGTCACCCCGAACAGGCTGTAAATCTG 2166
Db 2227 GAGCATGGGCTCTCGGGCTTCCACATTTGACCCGTCACCCCGAACAGGCTGTAAATCTG 2286
QY 2167 ATGCGCGACTTCTTTCGACCGGTGCAAGCAAGACCCAGATCCTGGGTGAATATCTGGA 2226
Db 2287 ATGCGCGACTTCTTTCGACCGGTGCAAGCAAGACCCAGATCCTGGGTGAATATCTGGA 2346
QY 2227 GCAGGCTCAGCGCATATACGAGAGATGACATGGAAGATATACTCAGAGAGCTTGATG 2286
Db 2347 GCAGGCTCAGCGCATATACGAGAGATGACATGGAAGATATACTCAGAGAGCTTGATG 2406
QY 2287 ACATGCGCGGGCTCTACGGTTTCTGGAAGTACGTCTCGAAGCTCGAGAGCTGGAGAGC 2346
Db 2407 ACATGCGCGGGCTCTACGGTTTCTGGAAGTACGTCTCGAAGCTCGAGAGCTGGAGAGC 2466
QY 2347 AGGCGCTACTTGGAGATGTTTCTACATCTGAGTTCGGGAGCTGCGGAGAGCGGTCCG 2406
Db 2467 AGGCGCTACTTGGAGATGTTTCTACATCTGAGTTCGGGAGCTGCGGAGAGCGGTCCG 2526
QY 2407 CTTCGAATTGACCAACCGCAGTAG 2430
Db 2527 CTTCGAATTGACCAACCGCAGTAG 2550

RESULT 3
AX756452/c
LOCUS 297 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 1191 from Patent WO03000905.
ACCESSION AX756452
VERSION AX756452.1 GI:32168583
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Ricke, D.
TITLE Identification and characterization of plant genes
JOURNAL Patent: WO 03000905-A 1191 03-JUN-2003;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers
1..297
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"
ORIGIN
Query Match 7.0%; Score 192; DB 6; Length 297;
Best Local Similarity 99.6%; Pred. No. 1.4e-89;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1393 GCTGATATATTCGTATGAACAATGCTGATTTTATCATCCAGACATACCAAGAAAT 1452
Db 243 GCTGATATATTCGTATGAACAATGCTGATTTTATCATCCAGACATACCAAGAAATC 184
QY 1453 GCTGGAAGCAAAAATACTGTTGACAGATGAGAGTCATGCTCTTACTCTGCTGGT 1512
Db 183 GCTGGAAGCAAAAATACTGTTGACAGATGAGAGTCATGCTCTTACTCTGCTGGT 124
QY 1513 CTGTACCGAGTTGTCCATGGGATCGATGCTTCGATCCAAAGTTCAATATGATCTCTCT 1572
Db 123 CTGTACCGAGTTGTCCATGGGATCGATGCTTCGATCCAAAGTTCAATATGATCTCTCT 64
QY 1573 GAGAGTGAATGTCATATATCTTTCCATACCGAGAGCGCAAGGACTCACTCTCTT 1632
Db 63 GAGAGTGAATGTCATATATCTTTCCATACCGAGAGCGCAAGGACTCACTCTCTT 4
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Query Match 4.4%; Score 122; DB 6; Length 265;

/note="Organ: leaf; genomic DNA from inbred line"
 <1..>222

STS
 ORIGIN
 Query Match 3.7%; Score 103; DB 11; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.5e-42;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2391 GCGAAGACCGTGGCGCTTGCATTCACCAACCGAGTAGCTTGGCAACTGGACTGGC 2450
 |||
 Db 119 GCGAAGACCGTGGCGCTTGCATTCACCAACCGAGTAGCTTGGCAACTGGACTGGC 178
 |||
 QY 2451 TAGCACTTGGTACAAGACTGAACCTGAGGAGCTTTCAGTAAT 2493
 |||
 Db 179 TAGCACTTGGTACAAGACTGAACCTGAGGAGCTTTCAGTAAT 221
 |||

RESULT 7
 BV079815
 LOCUS sc1180_p3 CML322 Zea mays CML322 Zea mays STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION BV079815
 VERSION BV079815.1 GI:37051472
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 225)
 REFERENCE
 AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 TITLE MPZ-UCI Joint SNP Discovery
 JOURNAL Unpublished (2003)
 COMMENT

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGGCGTACCTTGAGATGTTCTA
 Primer B: ATTATCAGCACTTCACCAAGTCC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase PS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 47 44 40 34 66 61 63 82 82 80 82 82
 87 81 85 81 77 76 81 84 80 73 73 88 90 90 82 70 70 73 85 81 90
 81 90 83 79 79 79 84 81 88 83 86 90 90 79 82 88 90 82 82 90 84
 83 79 81 81 81 74 83 83 82 8.

FEATURES
 source
 1..225
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="CML322"
 /db_xref="taxon:4577"
 /clone_lib="Zea mays CML322"

/dev_stage="seedling"
 /note="Organ: leaf; genomic DNA from inbred line"
 <1..>225

STS
 ORIGIN
 Query Match 3.7%; Score 103; DB 11; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.5e-42;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2391 GCGAAGACCGTGGCGCTTGCATTCACCAACCGAGTAGCTTGGCAACTGGACTGGC 2450
 |||
 Db 123 GCGAAGACCGTGGCGCTTGCATTCACCAACCGAGTAGCTTGGCAACTGGACTGGC 182
 |||
 QY 2451 TAGCACTTGGTACAAGACTGAACCTGAGGAGCTTTCAGTAAT 2493
 |||
 Db 183 TAGCACTTGGTACAAGACTGAACCTGAGGAGCTTTCAGTAAT 225
 |||

RESULT 8
 BV079813
 LOCUS sc1180_p3 CML333 Zea mays CML333 Zea mays STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION BV079813
 VERSION BV079813.1 GI:37051470
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 234)
 REFERENCE
 AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 TITLE MPZ-UCI Joint SNP Discovery
 JOURNAL Unpublished (2003)
 COMMENT

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGGCGTACCTTGAGATGTTCTA
 Primer B: ATTATCAGCACTTCACCAAGTCC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 37 44 40 29 29 29 42 42 44 77 73 60
 55 51 58 58 82 82 82 82 81 85 85 80 76 76 77 77 77 75 73 90
 90 90 83 63 63 62 71 83 90 77 81 87 82 84 81 81 81 83 86 81 90 90
 90 79 79 86 84 79 79 81 83 76 79 77 77 60 65.

FEATURES
 source
 1..234
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="CML333"
 /db_xref="taxon:4577"

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/db_xref="taxon:4577"
/clone_lib="Zea mays Kull11"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>234

STS
ORIGIN

Query Match      3.7%; Score 103; DB 11; Length 234;
Best Local Similarity 100.0%; Pred.No. 1.5e-42;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTCGCAACTGGCACTGCG 2450
      |||||
Db 132 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTCGCAACTGGCACTGCG 191
      |||||

QY 2451 TAGCACTTGTACAAAGACTGAACCTGAAGACCTTCAGTAAT 2493
      |||||
Db 192 TAGCACTTGTACAAAGACTGAACCTGAAGACCTTCAGTAAT 234
      |||||

RESULT 9
BV079812      239 bp      DNA      linear      STS 30-SEP-2003
LOCUS      sc1180_p3 Kull11 Zea mays Kull11 Zea mays STS genomic, sequence
DEFINITION      tagged_site.
ACCESSION      BV079812
VERSION      BV079812.1 GI:37051469
KEYWORDS      STS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 239)
AUTHORS      McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE      MPZ-UCI Joint SNP Discovery
JOURNAL      Unpublished (2003)
COMMENT      Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 32 32 28 28 56 70 74 67 63 75 61
75 81 77 76 62 60 54 67 62 90 88 84 82 82 90 81 90 87 82 81 76 81
81 77 77 77 83 90 90 79 71 71 79 83 79 90 90 89 84 84 84 89 84
80 80 80 86 90 87 87 87 90 79 79 87 86 82 90 90 81 81 7.

FEATURES
source
1..239
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Kull11"

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/db_xref="taxon:4577"
/clone_lib="Zea mays Kull11"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>239

STS
ORIGIN

Query Match      3.7%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred.No. 1.5e-42;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTCGCAACTGGCACTGCG 2450
      |||||
Db 137 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTCGCAACTGGCACTGCG 196
      |||||

QY 2451 TAGCACTTGTACAAAGACTGAACCTGAAGACCTTCAGTAAT 2493
      |||||
Db 197 TAGCACTTGTACAAAGACTGAACCTGAAGACCTTCAGTAAT 239
      |||||

RESULT 10
BV079814      239 bp      DNA      linear      STS 30-SEP-2003
LOCUS      sc1180_p3 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
DEFINITION      site.014
ACCESSION      BV079814
VERSION      BV079814.1 GI:37051471
KEYWORDS      STS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 239)
AUTHORS      McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE      MPZ-UCI Joint SNP Discovery
JOURNAL      Unpublished (2003)
COMMENT      Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 37 32 29 34 33 48 37 33 28 44 33 37
44 48 48 46 42 34 25 33 31 42 44 42 42 42 42 44 48 48 35 35 35
13 13 13 42 35 66 73 58 68 71 77 73 79 82 76 76 73 76 73 76 76
75 75 75 80 85 82 90 88 90 79 79 90 90 78 88 88 73 73 6.

FEATURES
source
1..239
/organism="Zea mays"
/mol_type="genomic DNA"

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/multivar="Oh43"
/db_xref="taxon:4577"
/clone_lib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>239
STS
ORIGIN

Query Match          3.7%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 GCGAAGACCGTGCCTTGCATTCACCAACCGAGTAGCTTGCGCAACTGGAGCTGG 2450
Db 137 GCGAAGACCGTGCCTTGCATTCACCAACCGAGTAGCTTGCGCAACTGGAGCTGG 196

QY 2451 TAGCACTTGGTACAGACTGAAACCTGAAGGACCTTCAGTAAT 2493
Db 197 TAGCACTTGGTACAGACTGAAACCTGAAGGACCTTCAGTAAT 239

RESULT 11
BV079819
LOCUS sc1180_p3 M37W Zea mays M37W DNA linear STS 30-SEP-2003
DEFINITION site.
ACCESSION BV079819
VERSION BV079819.1 GI:37051476
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 239)
REFERENCE
AUTHORS McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCAGTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 37 31 28 28 52 66 59 59 57 52 63 57
75 77 73 75 67 61 67 65 82 84 84 82 90 90 86 86 82 81 82
90 80 76 76 76 87 89 90 90 82 88 84 90 82 83 90 82 77 74 75 80
85 80 80 82 79 79 77 80 86 84 82 82 90 87 83 79 81 81 7.
FEATURES
source
Location/Qualifiers
1..239
/organism="Zea mays"

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/mol_type="genomic DNA"
/cultivar="M37W"
/db_xref="taxon:4577"
/clone_lib="Zea mays M37W"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>239
STS
ORIGIN

Query Match          3.7%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 GCGAAGACCGTGCCTTGCATTCACCAACCGAGTAGCTTGCGCAACTGGAGCTGG 2450
Db 137 GCGAAGACCGTGCCTTGCATTCACCAACCGAGTAGCTTGCGCAACTGGAGCTGG 196

QY 2451 TAGCACTTGGTACAGACTGAAACCTGAAGGACCTTCAGTAAT 2493
Db 197 TAGCACTTGGTACAGACTGAAACCTGAAGGACCTTCAGTAAT 239

RESULT 12
BV079818
LOCUS sc1180_p3 Ky21 Zea mays Ky21 DNA linear STS 30-SEP-2003
DEFINITION site.
ACCESSION BV079818
VERSION BV079818.1 GI:37051475
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 240)
REFERENCE
AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCAGTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 46 42 34 34 56 73 64 63 61 71 61 66
63 67 75 74 66 74 76 85 73 90 90 90 82 77 90 87 83 71 80
82 80 73 73 88 90 90 82 82 71 85 85 74 90 90 84 84 77 75 75
77 72 77 85 80 79 81 84 86 90 85 85 84 84 85 90 90 87 7.
FEATURES
source
Location/Qualifiers
1..240

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STs
ORIGIN

1. .>240

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Ky21"
/db_xref="taxon:4577"
/clone_lib="Zea mays Ky21"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"

Query Match 2.6%; Score 72; DB 11; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.6e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2422 CCGCAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGG 2481
|||||
Db 169 CCGCAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGG 228
|||||

QY 2482 ACCTTCAGTAAT 2493
|||||
Db 229 ACCTTCAGTAAT 240
|||||

RESULT 13
BV079820 234 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Hp301 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV079820
VERSION BV079820.1 GI:37051477
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 234)
AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
TITLE MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACAGTGCC
Protocol:

PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul

Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 52 66 62 61 67 65 61 61 61 69 71 73 63
66 64 72 72 87 88 84 80 80 85 84 81 76 77 80 71 73 70 84
79 79 79 78 67 81 85 90 81 85 83 77 72 69 69 77 77 75 85 80
79 90 90 90 90 81 81 84 84 82 90 90 79 77 70 75.
Location/Qualifiers

source

1. .>234

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Hp301"
/db_xref="taxon:4577"
/clone_lib="Zea mays Hp301"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"

STs
ORIGIN

Query Match 2.5%; Score 69; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.4e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2425 CAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGGACC 2484
|||||
Db 166 CAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGGACC 225
|||||

QY 2485 TTCAGTAAT 2493
|||||
Db 226 TTCAGTAAT 234
|||||

RESULT 14
BV079821 246 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 CML247 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV079821
VERSION BV079821.1 GI:37051478
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
TITLE MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACAGTGCC
Protocol:

PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul

Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 37 34 34 42 42 42 42 42 42 26 26
26 37 35 34 34 52 50 61 82 73 78 71 71 77 70 82 82 79 66 58 58
58 55 63 63 80 80 84 75 70 66 61 56 61 61 67 67 84 84 79 90 83
81 87 77 81 81 79 82 82 87 77 82 90 82 82 84 79 77 77 83 81 71
Location/Qualifiers

83 80 71 66 60.
FEATURES Location/Qualifiers
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STS
ORIGIN

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Best Local Similarity 100.0%; Pred.No.1.4e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2425 CAGTAGCTTGGCGCACTGGCGACTGGCTAGCACTTGGTACAGACTGAACCTGAAGGACC 2484
Db 178 CAGTAGCTTGGCGCACTGGCGACTGGCTAGCACTTGGTACAGACTGAACCTGAAGGACC 237
QY 2485 TTCAGTAAT 2493
Db 238 TTCAGTAAT 246

Search completed: May 26, 2004, 06:45:32
Job time : 7063.61 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:31:02 ; Search time 695.021 Seconds
(without alignments)
16851.697 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

Sequence: 1 atgtctgccgaagtga.....aaaaaaagggcgccgc 2757

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 212409941 residues

Word size : 50

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002s: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2757	100.0	2757	6	AAD45856 Corn Sus3
2	2571	93.3	2737	6	AAD45849 Corn suc
3	278	10.1	428	8	ADA58861 Maize suc
4	255	9.2	303	8	ADA58379 Maize suc
5	246	8.9	347	6	AAD45857 Sorghum p
6	209	7.6	283	8	ADA58372 Maize suc
7	192	7.0	297	9	ADC08886 Corn DNA
8	191	6.9	258	9	ADC08843 Corn DNA
9	159	5.8	285	8	ADA58359 Maize suc
10	158	5.7	297	8	ADA58362 Maize suc
11	150	5.4	150	8	ADA58373 Maize suc
12	143	5.2	411	8	ADA58864 Maize suc
13	134	4.9	255	8	ADA58374 Maize suc
14	130	4.7	181	8	ADA58370 Maize suc
15	122	4.4	265	7	ABX83402 Corn ear-
16	114	4.1	310	8	ADA58369 Maize suc
17	99	3.6	148	8	ADA58371 Maize suc
18	83	3.0	137	8	ADA58375 Maize suc
19	63	2.3	264	8	ADA58368 Maize suc

ALIGNMENTS

RESULT 1
AAD45856 standard; DNA; 2757 BP.
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AC AAD45856;
XX
DT 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
XX
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; chimeric; gene; ds.
XX
OS Zea mays.
OS Sorghum propinquum.
OS Chimeric.
XX
FH Key Location/Qualifiers
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FT /product= "Corn Sus3-Sorghum EST chimeric protein"
FT misc_feature 1..39
FT /tag= b
FT /note= "Sorghum propinquum EST DNA"
FT misc_feature 40..2757
FT /tag= c
FT /note= "Corn Sus3 DNA"
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XX WO200267662-A1.
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XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
XX PI
XX WPI: 2002-691625/74.
XX P-PSDB; AAE28502.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.
XX
XX Claim 1; Page 116-119; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant.
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is Corn Sus3-Sorghum EST chimeric DNA. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
SQ Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;
Query Match 100.0%; Score 2757; DB 6; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCTGCCCGAAGCTGAACCGACGCGAGCATCCGGACCGCGTCGAGGACACCCCTC 60

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QY 181 GGGCTCGCGGAGGACCCCTTCCTGACAGCTCCCTCGCTCCGGCAGGAGGCGATCGTGTG 240
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RESULT 3
ADA58861
ID 58861 standard; cDNA; 428 BP.
XX ADA58861
AC ADA58861;
XX
XX 20-NOV-2003 (first entry)
XX
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XX
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XX triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
XX fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
XX phosphoglucosyltransferase; vacuolar hydrogen translocating pyrophosphatase;
XX pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
XX invertase; sucrose synthase; hexokinase; fructokinase;
XX nucleoside diphosphate kinase-kinase; NDP;
XX glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
XX uridine diphosphate-glucose pyrophosphorylase; maize.
XX

OS Zea mays.
XX US2003-35870-A1.
PN 17-JUL-2003.
XX 26-JAN-1999; 99US-00237183.
XX 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
XX 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
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PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
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PR 16-JUN-1998; 98US-0089524P.
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PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
XX 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX (CHEI/) CHEIKH N.
XX (FISH/) FISHER D K.
XX (LIU/) LIU J.
PR Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX New maize or soybean enzymes and nucleic acid molecules associated with
PT the sucrose pathway, useful for genome mapping, gene identification and
PT analysis, plant breeding, or preparation of constructs for plant gene
PT expression.
XX Claim 2; Page; 117pp; English.
XX The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait, the maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: the sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
XX
SQ Sequence 428 BP; 118 A; 95 C; 126 G; 89 T; 0 U; 0 Other;
Query Match 10.1%; Score 278; DB 8; Length 428;
Best Local Similarity 99.7%; Pred. No. 1.1e-99;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2218 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAAGATATCTACTCAGAG 2277
DB 63 ATATCTGAGCAGGGCTGCAGCGCATATACGAGAGTACACATGGAAGATATCTACTCAGAG 122
QY 2278 AGGTTGATGACATCGCGGGGTCTACGGTTTCTCGAAAGTACGTGTGGAAGTCGAGAG 2337
DB 123 AGGTTGATGACATCGCGGGGTCTACGGTTTCTCGAAAGTACGTGTGGAAGTCGAGAG 182
QY 2338 CTGGAGACGAGCGGCTACCTTGAGATGTTCTACATCTACTGAAGTCGCGAGTCGAGAG 2397
DB 183 CGGGAGACGAGCGGCTACCTTGAGATGTTCTACATCTACTGAAGTCGCGAGTCGCGAG 242
QY 2398 ACCGTGCGCTTGCAATTGACCAACCGAGTAGCTTGGCAACTGCGAGTCGAGTACT 2457

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Db      243 ACCGTCGCGCTTGCAATTCGACCAACCGCAGTAGCTTGCAGCACTGCAGTGCAGTCACT 302
Qy      2458 TGGTACAGACTGAACCTGAAGGACCTTCAGTAATTTAGGCGCGGCAGACGGTAGCCAA 2517
Db      303 TGGTACAGACTGAACCTGAAGGACCTTCAGTAATTTAGGCGCGGCAGACGGTAGCCAA 362
Qy      2518 TAAATGTCGGGACCTGAACCTGGTTTTT 2546
Db      363 TAAATGTCGGGACCTGAACCTGGTTTTT 392

RESULT 4
ID ADA58379
XX AC ADA58379;
XX DT 20-NOV-2003 (first entry)
XX DE Maize sucrose synthase EST #23.
XX KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
XX KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
XX KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
XX KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
XX KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
XX KW invertase; sucrose synthase; hexokinase; fructokinase;
XX KW nucleoside diphosphate kinase-kinase; NDP;
XX KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
XX KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX QS Zea mays.
XX FN US2003:3587C-A1.
XX PD 17-JUL-2003.
XX PF 26-JAN-1999; 99US-00237183.
XX PR 24-NOV-1997; 97US-0067000P.
XX PR 09-DEC-1997; 97US-0069472P.
XX PR 27-JAN-1998; 98US-0072888P.
XX PR 10-FEB-1998; 98US-0074201P.
XX PR 10-FEB-1998; 98US-0074280P.
XX PR 10-FEB-1998; 98US-0074281P.
XX PR 10-FEB-1998; 98US-0074282P.
XX PR 12-FEB-1998; 98US-0074565P.
XX PR 12-FEB-1998; 98US-0074566P.
XX PR 12-FEB-1998; 98US-0074567P.
XX PR 19-FEB-1998; 98US-0074789P.
XX PR 19-FEB-1998; 98US-0075459P.
XX PR 19-FEB-1998; 98US-0075460P.
XX PR 19-FEB-1998; 98US-0075461P.
XX PR 19-FEB-1998; 98US-0075462P.
XX PR 19-FEB-1998; 98US-0075463P.
XX PR 06-MAR-1998; 98US-0075464P.
XX PR 09-MAR-1998; 98US-0076912P.
XX PR 09-MAR-1998; 98US-0077229P.
XX PR 09-MAR-1998; 98US-0077230P.
XX PR 18-MAR-1998; 98US-0077231P.
XX PR 07-APR-1998; 98US-0078368P.
XX PR 27-APR-1998; 98US-0080844P.
XX PR 29-APR-1998; 98US-0083067P.
XX PR 29-APR-1998; 98US-0083866P.
XX PR 29-APR-1998; 98US-0083867P.
XX PR 29-APR-1998; 98US-0083868P.
XX PR 29-APR-1998; 98US-0083869P.
XX PR 13-MAY-1998; 98US-0083900P.
XX PR 13-MAY-1998; 98US-0085222P.
XX PR 13-MAY-1998; 98US-0085223P.
XX PR 13-MAY-1998; 98US-0085224P.
XX PR 21-MAY-1998; 98US-0086183P.

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PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0096667P.
PR 09-SEP-1998; 98US-0096670P.
PR 09-SEP-1998; 98US-0096677P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101133P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108969P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.

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(CHRI/) CHEIKH N.
(FISH/) FISHER D K.
(LIU/) LIU J.

Cheikh N, Fisher DK, Liu J;

WPI; 2003-688722/65.

New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression.

Claim 2; Page; 117pp; English.

The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from: triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase, vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent fructose-6-phosphate phosphotransferase, invertase, sucrose synthase, hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase, glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine diphosphate (UDP)-glucose pyrophosphorylase. Also included are a substantially purified maize or soybean enzyme (or its fragment) and a transformed plant having a nucleic acid molecule. Also disclosed as new are purified antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway enzyme in a plant cell or plant tissue, determining a mutation in a plant whose presence is predictive of a mutation affecting the level or pattern

CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
XX
SQ Sequence 303 BP; 71 A; 78 C; 86 G; 68 T; 0 U; 0 Other;

Query Match 9.2%; Score 255; DB 8; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1761 GCTGCTGAGAGCTTTTGTCTAAGTCGGCTAAGCTGAGGAGCTGTAAACCTTGTCTCGT 1820
DB 1 GCTGCTGAGAGCTTTTGTCTAAGTCGGCTAAGCTGAGGAGCTGTAAACCTTGTCTCGT 60
QY 1821 TGCCGGGTACAATGATGTCAACAGTCCAAAGGACAGGGAAGAGATCGCGAGATAGAGAA 1880
DB 61 TGCCGGGTACAATGATGTCAACAGTCCAAAGGACAGGGAAGAGATCGCGAGATAGAGAA 120
QY 1881 GATGCTGAACTCATCAGACCCCAACTTTTTCGGGAGTTCGCTGGATCTCTGCCCA 1940
DB 121 GATGCTGAACTCATCAGACCCCAACTTTTTCGGGAGTTCGCTGGATCTCTGCCCA 180
QY 1941 GACAAACAGGGCCCGTAAACGGGAGCTTATCGCTACATCGCTGATACCCATGTGCTTT 2000
DB 181 GACAAACAGGGCCCGTAAACGGGAGCTTATCGCTACATCGCTGATACCCATGTGCTTT 240
QY 2001 CGTACAGCCGCGCTT 2015
DB 241 CGTACAGCCGCGCTT 255

RESULT 5
AAD45857
ID AAD45857 standard; DNA; 347 BP.
XX
AC AAD45857;
XX
DT 27-DEC-2002 (first entry)
XX
DE Sorghum propinquum EST DNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sush1;
KW transgenic plant; plant breeding; grain breakage; grain strength; EST;
KW cellulose; gene; Gs.
XX
OS Sorghum propinquum.
XX
PN W0200267662-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005137.
XX
PR 22-FEB-2001; 2001US-0270777P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Dhugga KS, Helentjaris TG, Niu X;
XX
DR WPI; 2002-691625/74.
XX
PT New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving

PT plant or grain strength.
XX
XX Example 11; Page 121; 125pp; English.
XX
CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
CC constitutive sucrose synthase (Sush1) and their corresponding nucleic
CC acids. The polynucleotide, or its encoded protein, is useful for
CC modulating the level of sucrose synthase in a transgenic plant,
CC increasing cellulose production in the stalk tissue of a transgenic
CC plant, or increasing the concentration of cellulose in the tissues of a
CC seed of a transgenic plant. This is particularly useful in plant (e.g.
CC maize or soybean) breeding, especially for e.g. improving stalk length in
CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is Sorghum propinquum EST DNA used in the exemplification of the
CC invention
XX
SQ Sequence 347 BP; 60 A; 141 C; 109 G; 37 T; 0 U; 0 Other;

Query Match 8.9%; Score 246; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.8e-87;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCTGCCCGAAGCTCAACGCAACGCGAGCATCCGGGACCGGTCGAGGACACCTTC 60
DB 102 ATGTCTGCCCGAAGCTCAACGCAACGCGAGCATCCGGGACCGGTCGAGGACACCTTC 161
QY 61 CACGGGACCCGCAAGAGCTGTGCGCTCTCTCCAAAGTACGTGAACAGGGGAGGGC 120
DB 162 CACGGGACCCGCAAGAGCTGTGCGCTCTCTCCAAAGTACGTGAACAGGGGAGGGC 221
QY 121 ATCTCTGAGCGCGACCATCTCGACGCGCTCGACGAGTCCAGGGTCCGGGGTCCGC 180
DB 222 ATCTCTGAGCGCGACCATCTCGACGCGCTCGACGAGTCCAGGGTCCGGGGTCCGC 281
QY 181 GCGCTCGCGGAGGAGCCCTTCTCGACGCTCTCTCGCTCCCGGACAGGAGCGATCGTGTG 240
DB 282 GCGCTCGCGGAGGAGCCCTTCTCGACGCTCTCTCGCTCCCGGACAGGAGCGATCGTGTG 341
QY 241 CCGCGC 246
DB 342 CCGCGC 347

RESULT 6
ADA58372
ID ADA58372 standard; cDNA; 283 BP.
XX
AC ADA58372;
XX
DT 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #16.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-A1.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 99US-00237183.
XX
PR 24-NOV-1997; 97US-0067000P.

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PR 09-DEC-1997; 98US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083389P.
PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089733P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0093170P.
PR 26-JUN-1998; 98US-0093288P.
PR 29-JUN-1998; 98US-0091335P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
PR 09-SEP-1998; 98US-0099672P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 18-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.

XX (CHEL/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
XX
XX Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX
XX New maize or soybean enzymes and nucleic acid molecules associated with
PT the sucrose pathway, useful for genome mapping, gene identification and
PT analysis, plant breeding, or preparation of constructs for plant gene
XX expression.
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XX Claim 2; Page; 117pp; English.
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XX The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucosomerase,
CC vacuolar hydrogen translocating-phosphatase, pyrophosphatase, fructose
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
XX
XX Sequence 283 BP; 75 A; 74 C; 67 G; 67 T; 0 U; 0 Other;
SQ

Query Match 7.6%; Score 209; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.9e-72;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 CCAAGTTCATATAGTCTCTCTCTGGAGCTGACATGTCATATACCTTCCACATACCGAG 1608
Db 9 CCAAGTTCATATAGTCTCTCTCTGGAGCTGACATGTCATATACCTTCCACATACCGAG 68
QY 1609 AAGGCCAAGCGACTCACCTCTCTTCATGGTTCATCGAAATTTGATTTATGACCGGAG 1668
Db 69 AAGGCCAAGCGACTCACCTCTCTTCATGGTTCATCGAAATTTGATTTATGACCGGAG 128
QY 1669 CAAACGATGACACATTTGGGCACTTGGATGACCGGTCAAGCCCATCTCTTCTTCATG 1728
Db 129 CAAACGATGACACATTTGGGCACTTGGATGACCGGTCAAGCCCATCTCTTCTTCATG 188
QY 1729 GCAAGACTCGACAGGTTGAAGACATAAC 1757
Db 189 GCAAGACTCGACAGGTTGAAGACATAAC 217

RESULT 7
ADC08886/c
ID ADC08886 standarç; DNA; 297 BP.
XX
AC ADC08886;
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QY 247 TTCGGGCGCATCGCGTGGCCGCGCCGCGGAGTTTGGAGTACGTCGCGTCAACGTT 306
 Db 198 TTCGGGCGCATCGCGTGGCCGCGCCGCGGAGTTTGGAGTACGTCGCGTCAACGTT 139
 QY 307 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGAGTACCTCGCTTCAAGGAGGAGCTT 366
 Db 138 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGAGTACCTCGCTTCAAGGAGGAGCTT 79
 QY 367 GTCGACGGCCA 377
 Db 78 GTCGACGGCCA 68

RESULT 9
 ADA58359 ID ADA58359 standard; cDNA; 285 BP.
 XX AC ADA58359;
 XX AC
 DT 20-NOV-2003 (first entry)
 XX DE Maize sucrose synthase EST #3.
 XX DE
 KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
 KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-Kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucose mutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.
 XX Zea mays.
 XX
 PN US2003135870-A1.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-JAN-1999; 99US-00237183.
 XX
 PR 24-NOV-1997; 97US-0067000P.
 PR 09-DEC-1997; 97US-0069472P.
 PR 27-JAN-1998; 98US-0072888P.
 PR 10-FEB-1998; 98US-0074201P.
 PR 10-FEB-1998; 98US-0074280P.
 PR 10-FEB-1998; 98US-0074281P.
 PR 10-FEB-1998; 98US-0074282P.
 PR 12-FEB-1998; 98US-0074565P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
 PR 19-FEB-1998; 98US-0074789P.
 PR 19-FEB-1998; 98US-0075459P.
 PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
 PR 19-FEB-1998; 98US-0075463P.
 PR 19-FEB-1998; 98US-0075464P.
 PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077229P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
 PR 29-APR-1998; 98US-0083386P.
 PR 29-APR-1998; 98US-0083387P.
 PR 29-APR-1998; 98US-0083388P.
 PR 29-APR-1998; 98US-0083389P.
 PR 29-APR-1998; 98US-0083390P.
 PR 13-MAY-1998; 98US-0085222P.
 PR 13-MAY-1998; 98US-0085223P.
 PR 13-MAY-1998; 98US-0085224P.

PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089810P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0099667P.
 PR 09-SEP-1998; 98US-0099670P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101134P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 22-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 98US-00229413.

(CHEI/) CHEIKH N.
 (FISH/) FISHER D K.
 (LIU/) LIU J.

Cheikh N, Fisher DK, Liu J;
 WPI; 2003-688722/65.

New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression.

Claim 2; Page; 117pp; English.

The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from: triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase, vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent fructose-6-phosphate phosphotransferase, invertase, sucrose synthase, hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase, glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine diphosphate (UDP)-glucose pyrophosphorylase. Also included are a substantially purified maize or soybean enzyme (or its fragment) and a transformed plant having a nucleic acid molecule. Also disclosed as new are purified antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway enzyme in a plant cell or plant tissue, determining a mutation in a plant

CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
 XX
 SQ Sequence 285 BP; 64 A; 82 C; 76 G; 63 T; 0 U; 0 Other;

Query Match 5.8%; Score 159; DB 8; Length 285;
 Best Local Similarity 100.0%; Pred. No. 9.8e-53;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1857 GGAAGAGATCGCGAGATAGAGATGCGTCACTGATCAAGACCCCAACTTGTTCGG 1916
 Db 1 GGAAGATCGCGAGATAGAGATGCGTCACTGATCAAGACCCCAACTTGTTCGG 60
 QY 1917 GCAGTTCGCTGGATCTCTGCCAGACAAACAGGCGCGTAAACGCGAGCTCTATCGCTA 1976
 Db 61 GCAGTTCGCTGGATCTCTGCCAGACAAACAGGCGCGTAAACGCGAGCTCTATCGCTA 120
 QY 1977 CATCGGTATACCATGGTGTCTTTCGTACACCGCGCTT 2015
 Db 121 CATCGGTATACCATGGTGTCTTTCGTACACCGCGCTT 159

RESULT 10

ADAS8362

ID ADA58362 standard; cDNA; 297 BP.

XX AC ADA58362;

XX DT 20-NOV-2003 (first entry)

XX DE Maize sucrose synthase EST #6.

XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
 KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX OS Zea mays.

XX US2003135870-A1.

XX PD 17-JUL-2003.

XX PF 26-JAN-1999; 99US-00237183.

XX 24-NOV-1997; 97US-0067000P.

XX 09-DEC-1997; 97US-0069472P.

XX 27-JAN-1998; 98US-0072888P.

XX 10-FEB-1998; 98US-0074201P.

XX 10-FEB-1998; 98US-0074280P.

XX 10-FEB-1998; 98US-0074281P.

XX 12-FEB-1998; 98US-0074282P.

XX 12-FEB-1998; 98US-0074565P.

XX 12-FEB-1998; 98US-0074566P.

XX 19-FEB-1998; 98US-0074789P.

XX 19-FEB-1998; 98US-0075459P.

PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
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 PR 06-MAR-1998; 98US-0076912P.
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 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108966P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.

(CHEI/) CHEIKH N.

PA (FISH/) FISHER D K.

PA (LIUJ/) LIU J.

PI Cheikh N, Fisher DK, Liu J;

XX WPI; 2003-688722/65.

XX New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and

PT analysis, plant breeding, or preparation of constructs for plant gene
PT expression.
XX
BS
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CC The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
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CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
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CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
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CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
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CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX Sequence 297 BP; 92 A; 51 C; 65 G; 89 T; 0 U; 0 Other;

Query Match 5.7%; Score 158; DB 8; Length 297;

Best Local Similarity 99.2%; Pred. No. 2.4e-52;

Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1122 TAAGAAATGATATCAGATTTCATGTCGTCATATCTGCGCATATCTGGAACATTTCTGAGGATGC 1181

Db 2 TAAGAAATGATATCAGATTTCATGTCGTCATATCTGCGCATATCTGGAACATTTCTGAGGATGC 61

QY 1182 TGTCTGTAATTCCTCTCAATTAACAAGTACTCCAGACTTCATATTTGGAACATACAG 1241

Db 62 TGTCTGTAATTCCTCTCAATTAACAAGTACTCCAGACTTCATATTTGGAACATACAG 121

QY 1242 TGATGAAATCTTGTGGCGTCATTTGCTATCTTACAAGATGGGAATACCCAGTGCACAT 1301

Db 122 TGATGAAATCTTGTGGCGTCATTTGCTATCTTACAAGATGGGAATACCCAGTGCACAT 181

QY 1302 TGCTCATGCTCGAAAGACTAGTATCCAGATTCAGACATATTTGGGAAGATTTGGA 1361

Db 182 TGCTCATGCTCGAAAGACTAGTATCCAGATTCAGACATATTTGGGAAGATTTGGA 241

QY 1362 TGAGAGTACCATTTCTCT 1381

Db 242 TGAGAGTACCATTTCTCT 261

RESULT 11

ADA58373

ID ADA58373 standard; cDNA; 150 BP.

XX

AC ADA58373;

XX

DT 20-NOV-2003 (first entry)

XX

DE Maize sucrose synthase EST #17.

XX

KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;

KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;

KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
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OS Zea mays.

XX US2003135870-A1.

PN 17-JUL-2003.

PD 26-JAN-1999;

PF 99US-00237183.

XX 97US-0067000P.

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PR 98US-0075459P.

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PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
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 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-02199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.
 XX

PA (CHEI/) CHEIKH N.
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 XX WPI; 2003-688722/65.

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 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
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 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
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 CC transformed plant having a nucleic acid molecule. Also disclosed as new
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 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
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 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
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 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.htc-1?DocID=20030135870.

XX Sequence 150 BP; 39 A; 39 C; 29 G; 43 T; 0 U; 0 Other;

Query Match 5.4%; Score 150; DB 8; Length 150;
 Best Local Similarity 100.0%; Pred. No. 3.8e-49;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 ACCGAGTGTCCATGATCTTCGATCCAGAGTCAATATAGTCTCTCTGAG 1576
 |||||
 Db 1 ACCGAGTGTCCATGATCTTCGATCCAGAGTCAATATAGTCTCTCTGAG 60
 |||||

QY 1577 CTGACATGTCCATATCTTTCCATACCGAGAGGCCAAGCGACTCACCTCTCTCATG 1636

Db 61 CTGACATGTCCATATCTTTCCATACCGAGAGGCCAAGCGACTCACCTCTCTCATG 120
 |||||
 QY 1637 GTTCAATCGAAATTTGATTTATGACCCGG 1666
 |||||
 Db 121 GTTCAATCGAAATTTGATTTATGACCCGG 150
 |||||

RESULT 12

ADA58864
 ID ADA58864 standard; cDNA; 411 BP.

AC ADA58864;

XX 20-NOV-2003 (first entry)

XX Maize sucrose synthase EST #508.

XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX Zea mays.

XX US2003135870-A1.

XX 17-JUL-2003.

XX 26-JAN-1999; 99US-00237183.

XX 24-NOV-1997; 97US-0067000P.

XX 09-DEC-1997; 97US-0069472P.

XX 27-JAN-1998; 98US-0072888P.

XX 10-FEB-1998; 98US-0074201P.

XX 10-FEB-1998; 98US-0074281P.

XX 12-FEB-1998; 98US-0074282P.

XX 12-FEB-1998; 98US-0074565P.

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XX 19-FEB-1998; 98US-0075463P.

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XX 06-MAR-1998; 98US-0076912P.

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PR 22-SEP-1998; 98US-0101344P.
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PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0112244P.
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CC The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or

CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
XX
SQ Sequence 411 BP; 99 A; 109 C; 113 G; 88 T; 0 U; 2 Other;
Query Match 5.2%; Score 143; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1759 GGGCTGGTCAAGCTTTTCTAAGTCGGCTAAGTCAGGAGCTGTAAACCTTTCGTC 1818
DB 88 GGGCTGGTCAAGCTTTTCTAAGTCGGCTAAGTCAGGAGCTGTAAACCTTTCGTC 147
QY 1819 GTTCCGGGTACAAATGATCTCAACAGTCCAGGACAGGAGAGATCGCGGAGATAGAG 1878
DB 148 GTTCCGGGTACAAATGATCTCAACAGTCCAGGACAGGAGAGATCGCGGAGATAGAG 207
QY 1879 AAGATGCATGAACCTCATCAAGAC 1901
DB 208 AAGATGCATGAACCTCATCAAGAC 230
RESULT 13
ADA58374
ID ADA58374 standard; cDNA; 255 BP.
XX
AC ADA58374;
XX
DT 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #18.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucose mutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-A1.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 98US-00237183.
XX
PR 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 12-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
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PR 19-FEB-1998; 98US-0075464P.

PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077229P.
 PR 09-MAR-1998; 98US-0077230P.
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 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
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 PR 13-MAY-1998; 98US-0085224P.
 PR 21-MAY-1998; 98US-0086183P.
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 PR 01-JUN-1998; 98US-0087422P.
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 PR 25-JUN-1998; 98US-0090282P.
 PR 29-JUN-1998; 98US-0091035P.
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 PR 08-JUL-1998; 98US-0092036P.
 PR 03-SEP-1998; 98US-0099667P.
 PR 03-SEP-1998; 98US-0099670P.
 PR 03-SEP-1998; 98US-0099697P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210257.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.
 PR (CHEI/) CHEIKH N.
 PR (FISH/) FISHER D K.
 PR (LIUJ/) LIU J.
 PR Cheikh N, Fisher DK, Liu J;
 PR WPI; 2003-688722/65.
 PR New maize or soybean enzymes and nucleic acid molecules associated with
 PR the sucrose pathway, useful for genome mapping, gene identification and
 PR analysis, plant breeding, or preparation of constructs for plant gene
 PR expression.
 PR Claim 2; Page: 117pp; English.
 PR XX

CC The invention relates to a substantially purified nucleic acid molecule
 CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC transformed plant having a nucleic acid molecule. Also disclosed as new
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
 CC XX
 CC SQ Sequence 255 BP; 63 A; 62 C; 67 G; 63 T; 0 U; 0 Other;

Query Match 4.9%; Score 134; DB 8; Length 255;
 Best Local Similarity 100.0%; Pred. No. 7.2e-43;
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 584 ATGATAGATACAAAGCTTGGGAGGCTTCAGTCTGTCTGACCAAAAGCTGAGGAGCACT 643
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 Db 110 ATGATAGATACAAAGCTTGGGAGGCTTCAGTCTGTCTGACCAAAAGCTGAGGAGCACT 169
 |||||

Cy 644 TGTCAAAGCTCCCTGCTGACACACCACTACTCACAATTGCTTATAAATTTCAAGATGGG 703
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 Db 170 TGTCAAAGCTCCCTGCTGACACACCACTACTCACAATTGCTTATAAATTTCAAGATGGG 229
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Cy 704 GCCTGGAGAAAAGGT 717
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 Db 230 GCCTGGAGAAAAGGT 243
 |||||

RESULT 14
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 ID ADA58370 standard; cDNA; 181 BP.
 XX ADA58370;
 AC ADA58370;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Maize sucrose synthase EST #14.
 XX
 KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDF;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.
 XX Zea mays.
 XX
 XX OS
 XX
 XX US2003135870-A1.
 XX
 XX 17-JUL-2003.

ABX83402
ID ABX83402 standard; cDNA; 265 BP.

XX

AC ABX83402;

XX

DT 24-APR-2003 (first entry)

XX

XX Corn ear-derived polynucleotide (cpd) #1862.

XX

KW Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
KW structural gene; functional gene; regulatory gene;
KW corn ear-specific profile; gene transcription; gene expression;
KW hybrid plant; desirable trait expression; plant breeding program;
KW inheritance; desired characteristic; growth; development;
KW disease resistance; environmental adaptability; quality; yield;
KW multigene trait; plant; gene; ss.

XX

OS Zea mays.

XX

XX US6476212-B1.

XX

PD 05-NOV-2002.

XX

PF 14-MAY-1999; 99US-00313294.

XX

PR 26-MAY-1998; 98US-0086722P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lalgudi RV, Ito LY, Sherman BK;

XX

DR WPI; 2003-208840/20.

XX

PT Novel purified corn-ear derived polynucleotide useful as hybridization
PT probe for detecting polynucleotide in sample, and for identifying,
PT evaluating, and altering desired characteristics associated with growth,
PT development.

XX

PS Example; SEQ ID NO 1862; 390pp; English.

XX

CC The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and SATMON023. Some of the cdps uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotides sequences are
CC useful for detecting cdps in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC inbred or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cdps are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridisation techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cdps are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cdps are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cdps are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX81940 represent corn ear-derived
CC polynucleotides (cdps) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdIDentry.html

XX

SQ Sequence 265 BP; 65 A; 63 C; 71 G; 66 T; 0 U; 0 Other;

XX

Query Match 4.4%; Score 122; DB 7; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.8e-35;
Matches 122; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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584 ATGATAGATACAAAGCTTGGGGAGGCTTCAGTCTGCTGCACCAAAAGCTGAGGAGCACT 643
|||||

Db 110 ATGATAGATACAAAGCTTGGGGAGGCTTCAGTCTGCTGCACCAAAAGCTGAGGAGCACT 169
Qy 644 TGTCAAAGCTCCCTGCTGACACACACACTACTCACAATTTGCTTATAAAATTCAGAGTGGG 703
Db 170 TGTCAAAGCTCCCTGCTGACACACACACTACTCACAATTTGCTTATAAAATTCAGAGTGGG 229
Qy 704 GC 705
Db 230 GC 231

Search completed: May 26, 2004, 02:50:35
Job time : 697.021 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n.mcdl
Run on: May 26, 2004, 12:48:39 ; Search time 100.937 Seconds
(without alignments)
4447.890 Million cell updates/sec

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Perfect score: 4247
Sequence: 1 MSAPKLNINASIRDRVEDTL.....YILKFKRELAKTVPALDQPO 809

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1363418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/prodata/2/ira/6D_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	3158	74.4	2563	2	US-08-553-436A-7
2	2892.5	68.1	3103	4	US-09-598-401C-57
3	2452	57.7	6386	2	US-08-483-376-1
4	1833	43.2	2700	4	US-08-684-025-1
5	444	10.5	3509	1	US-08-175-471-6
6	444	10.5	3509	3	US-08-718-777-6
7	444	10.5	3509	3	US-09-078-862-2
8	444	10.5	3509	3	US-09-251-341-6
9	444	10.5	3509	4	US-09-866-153-12
10	444	10.5	3509	4	US-09-693-467A-12
11	441.5	10.4	3625	1	US-08-356-354-3
12	441.5	10.4	3625	2	US-08-778-656-3

13	441.5	10.4	3635	2	US-08-553-436A-5	Sequence 5, Appli
14	436	10.3	3509	2	US-08-429-054A-12	Sequence 12, Appl
15	420	9.9	3524	4	US-09-697-367-15	Sequence 15, Appl
16	413.5	9.7	265	4	US-09-313-294A-1862	Sequence 1862, Ap
17	408	9.6	3539	3	US-08-853-948B-1	Sequence 1, Appli
18	396	9.3	3740	1	US-08-356-354-1	Sequence 1, Appli
19	396	9.3	3740	2	US-08-778-656-1	Sequence 1, Appli
20	365	8.6	271	4	US-09-313-294A-1826	Sequence 1826, Ap
21	355	8.4	532	4	US-09-598-401C-56	Sequence 56, Appl
22	328	7.7	272	4	US-09-313-294A-1221	Sequence 1221, Ap
23	307	7.2	2930	1	US-08-356-354-5	Sequence 5, Appli
24	307	7.2	2930	2	US-08-778-656-5	Sequence 5, Appli
25	297.5	7.0	1611	4	US-09-697-367-7	Sequence 7, Appli
26	282	6.6	2236	4	US-09-697-367-1	Sequence 1, Appli
27	186	4.4	210	3	US-09-125-384-1	Sequence 1, Appli
28	180.5	4.3	282	4	US-09-313-294A-427	Sequence 427, App
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30	175.5	4.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
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39	149.5	3.5	1110	4	US-09-543-681A-3342	Sequence 3342, Ap
40	148	3.5	1182	4	US-09-252-591A-2472	Sequence 2472, Ap
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C 42	142.5	3.4	42988	4	US-08-311-731A-128	Sequence 128, App
43	142	3.3	1065	2	US-08-512-955-1	Sequence 1, Appli
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45	134.5	3.2	1167	4	US-09-489-039A-999	Sequence 999, App

ALIGNMENTS

RESULT 1
US-08-553-436A-7
; Sequence 7, Application US/08553436A
; Patent No. 5866790
; GENERAL INFORMATION:
; APPLICANT: HESSE, Holger
; APPLICANT: MULLER-ROBER, Bernd
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
; TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
; TITLE OF INVENTION: CONCENTRATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oetrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,436A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/01671
; FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 4317596.1
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward
; REGISTRATION NUMBER: 24,735

REFERENCE/DOCKET NUMBER: P/951-117
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 382-0700
 TELEFAX: (212) 382-0888
 TELEX: 236925
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2563 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Beta vulgaris
 INDIVIDUAL ISOLATE: Saccharosynthese
 IMMEDIATE SOURCE:
 LIBRARY: phage lambda zap
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..2303
 US-08-553-436A-7

Alignment Scores:
 Pred. No.: 0 Length: 2563
 Score: 3158.00 Matches: 595
 Percent Similarity: 88.95% Conservative: 73
 Best Local Similarity: 79.23% Mismatches: 81
 Query Match: 74.36% Indels: 2
 DB: 2 Gaps: 2

US-10-080-114A-12 (1-809) x US-08-553-436A-7 (1-2563)

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 QY 78 IleValLeuProPheValAlaIleAlaValArgProArgProGlyValTrpGluTyr 97
 DB 69 ATAGTTGTTCCCTCCCTTTGTTGTTATAGCAGTCCGTCGAAGACCTGGAGTTGGGAATAT 128
 QY 98 ValArgValAsnValHisGluLeuSerValGluGlnLeuThrValSerGluTyrLeuArg 117
 DB 129 GTTCGGTTAAATGCTCTGAACACTGAATGTGGACGCTAACTGTGTGAGTATCTCCAT 188
 QY 118 PheLysGluGluValAspGlyGlnHisAsnAspProTyrValLeuGluLeuAspPhe 137
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 QY 138 GluProPheAsnValSerValProArgProAsnArgSerSerIleGlyAsnGlyWal 157
 DB 249 GAGCCCTTTAAATGAATCAGTTCACGCTCCACACTCGCTCTCATCAATTTGTAATGGTGT 308
 QY 158 GlnPheLeuAsnArgHisLeuSerSerIleMetPheArgAsnArgAspCysLeuGluPro 177
 DB 309 CAGTTCTCAATCGGCRCTGTCTCAGCATGTTCTGCAACAAGATTCITTTGAGCCG 368
 QY 178 LeuLeuAspPheLeuArgGlyHisArgHisLysGlyHisValMetMetLeuAsnAspArg 197
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 DB 429 ATACAGACTATTCAGGCTCTTCTCAGTCTGCATTTCTCTAAAGCTGAGGATTAICTTATCAA 488
 QY 218 LeuProAlaAspThrProTyrSerGlnPheAlaTyrLysPheGlnGluTrpGlyLeuGlu 237
 DB 489 CTTCCAGCAKATACACTTACTCTGAGTTCGAATTTGTATTCACAGGTATGGGTTTGA 548
 QY 238 LysGlyTrpGlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuAspIle 257
 DB 549 AGAGGCTGGGGTGATCTGCTGAAAGGGTCTTAGAAATGATGATCTACTAGATATC 608
 QY 258 IleGlnAlaProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIlePhe 277

DB 609 CTTTCAGGCTCCCGATCGTCTACATTAGAGACATTTCTGGGAACACTTCCCATGGTGT 668
 QY 278 AsnValValValValSerProHisGlyTyrPheGlyGlnAlaAsnValLeuGlyLeuPro 297
 DB 669 AATGTGCTCATTTTGTCTGTACATGGATATTTTGGACAGGCACATGTGCTGGCTGGCT 728
 QY 298 AspThrGlyGlyGlnIleValTyrIleLeuAspGlnValArgAlaLeuGluAsnGluMet 317
 DB 729 GACATGCTGGCGAGATAGTATTATCTTACCCAGTGGCTCTCTGGAAACATGAATG 788
 QY 318 ValLeuArgLeuLysLysGlnGlyLeuAspValSerProLysIleLeuIleValThrArg 337
 DB 789 CTCCAACGAATAAAGAACCAAGACATAGATGTGATCTCTAGAAATTTCTATCGTGAATCG 848
 QY 338 LeuIleProAspAlaLysGlyThrSerCysAsnGlnArgLeuGluArgIleSerGlyThr 357
 DB 849 TTGATTTCTGACGCTAAAGGACACACGTCATTCACGTATGGAGAAAGTCAGTGGAAACA 908
 QY 358 GlnHisThrTyrIleLeuArgValProPheArgAsnGluAsnGlyIleLeuLysLysTyr 377
 DB 909 GAGCATGCTAGTATCTGAGAGTTCCTTTCGATCAGAGAAAGAAATCTCTCCGCAATGG 968
 QY 378 IleSerArgPheAspValTrpProTyrLeuGluThrPheAlaGluAspAlaAlaGlyGlu 397
 DB 969 ATATCTAGATTTTCATGTATGCGCTTATTTAGAGACCTTCACTGAGGATGCGAGTGTGA 1028
 QY 398 IleAlaAlaGluLeuGlnGlyThrProAspPheIleIleGlyAsnTyrSerAspGlyAsn 417
 DB 1029 ATTATTGGCGAGTTGGAGGTCGTCAGATCTCATTAATTGGCAACTACACGCGATGGGAAT 1088
 QY 418 LeuValAlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAla 437
 DB 1089 ATAGTTGCTTCTTATTTGTCACCAAAATGGGTGTCACCCAGTGCATATATAGCCCATG 1148
 QY 438 LeuGluLysThrLysTyrProAspSerAspIlePheTrpLysAsnPheAspGluLysTyr 457
 DB 1149 TTGAGAAACCAAGTATCCAGATTCGATATTTACTGGAAAAAGATTGAGGACAAATAT 1208
 QY 458 HisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPheIle 477
 DB 1209 CACTTCGTTGTCATTTTCAGCTGACTTGGCAATGAATCATGCTGATTTTCATCAT 1268
 QY 478 ThrSerThrTyrGlnIleAlaGlySerLysAsnThrValGlyGlnTyrGluSerHis 497
 DB 1269 ACCGATCTTACCAAGAGATAGCTGGAAACGAAGATATCTTGGTCAATATGAAGCCAT 1328
 QY 498 ThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspValPheAspPro 517
 DB 1329 AAGGCTTTTACTTTTCGGGGCTGTATCGGTGCTTCAAGGATTTGATGCTTTGATCCC 1388
 QY 518 LysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGluLys 537
 DB 1389 AAGTTTAATATTGTCGCGAGGGGACATGCGCATCTTCTTCCATTTTTCAGAGAAG 1448
 QY 538 ---AlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu 556
 DB 1449 GATGTCCACCTGCTCACTTCACTTATAGAGCAGCTCTCTATTCAAACCTGAG 1508
 QY 557 GlnAsnAspGluHisIleGlyHisLeuAspAspArgSerLysProIleLeuPheSerMet 576
 DB 1509 CAGAACGAAGAACACATTTGGTGTATTAGATGTATCTCAAGCCAAATATTATTTCCATG 1568
 QY 577 AlaArgLeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAla 596
 DB 1569 GCGAGCTAGACGCTGGAAGAAATATACAGGCTCTGTAGAGTGTATGCGCAAGATGCG 1628
 QY 597 LysLeuArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSer 616
 DB 1629 AAATCAGGAACTGCAACCTGGTTGTAGTGGCTGGGTACATGATGATGATGATGATG 1688
 QY 617 LysAspArgGluIleAlaGluIleGluLysMetHisGluLeuIleLysThrHisAsn 636

1689 AATGACAGGAGGAAATTCGCCAAATCCGACAGATGACACAGGCTTATACAGGATATAAT 1748
Qy
637 LeuPheGlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeu 656
Db
1749 TTAAGAGGACAAATTCGCTGGATTCCTCAACAACAAATAGAGTACGAAATGGTGAACTC 1808
Qy
657 TyrArgTrpIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPhe 676
Db
1809 TATCGCTACATTTGTGACAAAGAGGATTTTTCGCGAGCTGCATTTATGAGCAATTT 1868
Qy
677 GlyLeuThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGly 696
Db
1869 GGGCTTACAGTTTGTGAAGCATGACCTGTGGTCTTCCACATTTGCTACTGCGCAGGT 1928
Qy
637 GlyProAlaGlnIleGluHisGlyValSerGlyPheHisIleAspProTyrHisPro 716
Db
1929 GGTCCAGCTGAGATATAGAAAGCGGTGTTTCAGGATTTTCATTCGATCCATATCATGCT 1988
Qy
717 GluGlnAlaValAsnLeuMetAlaAspPheAspArgCysLysGlnAspProAspHis 736
Db
1989 GATCAGCA---GAAAAATGACTGAATCTTTGTCAAGTGCAGAGAGATCCAACTAC 2045
Qy
737 TrpValAsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTrpLysIle 756
Db
2046 TGGACTAAATCTCTCGCAGGAGGTTACTAAGGATCAAGAAAGATATACCTGCGCAAAG 2105
Qy
757 TyrSerGluArgLeuMetThrLeuAlaGlyValTyrGlyPheTrpLysTyrValSerLys 776
Db
2106 TATTCGAAAGGTTATGACATTTGGCAGGGGTGATGGTTTCGGAATATGCTCTCAA 2165
Qy
777 LeuGluArgLeuGluThrArgArgTyrLeuGluMetPheTyrIleLeuLysPheArgGlu 796
Db
2166 CTAGAGAGAGAGACAGACAGCTTATCTTGAGATGTTCTACATTTGAAATTCCTGGAT 2225
Qy
797 LeuAlaLysThrValProLeuAlaIleAspGln 807
Db
2226 CTGGCCAACTCTGTCGCTGGCAACAGATGAA 2258

RESULT 2

US-09-598-401C-57
; Sequence 57, Application: US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Ragneton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.10362
; CURRENT APPLICATION NUMBER: US/09/598,401C
; PRIORITY FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 3103
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-57

Alignment Scores:
Pred. No.: 0 Length: 3103
Score: 2892.50 Matches: 540
Percent Similarity: 81.78% Conservative: 120
Best Local Similarity: 66.91% Mismatches: 144
Query Match: 68.11% Indels: 3
DB: 4 Gaps: 2

US-10-080-114A-12 (1-809) x US-09-598-401C-57 (1-3103)
Qy 1 MetSerAlaProLysLeuAsnArgAsnAlaSerIleArgAspArgValGluAspThrLeu 20
Db 447 ATGCTCATGTCATGTTGACTCGAAGCCACACAGCTTCGCGAGCGTTTGGAGAGACCCCTC 506
Qy 21 HisAlaHisArgAndIleLeuValAlaLeuLeuSerLysTyrValAsnLysGlyLysGly 40
Db 507 TCTGCTCAGCCACAGATTTGCGCTTCCTTTCAAGGGTTGAAGCCCAAGCAAGAGC 566
Qy 41 IleLeuGlnProHisHisIleLeuAspAlaLeuAspGluValGlnGlnGlySerGlyValArg 60
Db 567 ATCTTGACGCCACAGATTTTGTGAGTTTGAGCCATCTCTGAGGAGAGCAGAGCA 626
Qy 61 AlaLeuAlaGluGlyPropheLeuAspValLeuArgSerAlaGlnGluAlaIleValLeu 80
Db 627 AAGCTTCTTATGATGGGCTTTGGTGAAGTCTCAATTCACCTCAGGAAGCGATTTGTGTCG 686
Qy 81 ProProPheValAlaIleAlaValArgProArgProGlyValTrpGluTyrValArgVal 100
Db 687 CTTCCATGGGTGCTCTGTGTTCTGTCAGAGCGGGCGTGTGGAGACATCCGTTG 746
Qy 101 AsnValHisGluLeuSerValGluGlnLeuThrValSerGluTyrLeuArgPheLysGlu 120
Db 747 AAGTCTCATGCGCTTGTCTTGACCAATTTGAGGTTCCTGAGTATCTGCACCTCAAGAA 806
Qy 121 GluLeuValAspGlyGlnHisAsnAspProTyrValLeuGluLeuAspPheGluProPhe 140
Db 807 GAGCTTCTCATGGAAGCTTGAATGGTAACCTTTGCTTGAGCTTGACTTTGAGCCATTC 866
Qy 141 AsnValSerValProArgProAsnArgSerSerIleGlyAsnGlyValGlnPheLeu 160
Db 867 ACTGCTCTTTTTCGCGCCGACTCTTTTCCAGTCTATTTGCAATGGCGTGGATTTCTC 926
Qy 161 AsnArgHisLeuSerSerIleMetPheArgAsnArgCysLysLeuGluProLeuLeuAsp 180
Db 927 AATGCGCATCTCTCGCTAAGCTCTTCCATGACAAAGAAAGCTTGCACCTCTGCTGAA 986
Qy 181 PheLeuArgGlyHisArgHisLysGlyHisValMetMetLeuAsnAspArgIleGlnSer 200
Db 987 TTCTTCCAGTCCACTGCTCAAGGGGAAGAACATGATGTTGAATGCCAGAATCCAGAT 1046
Qy 201 LeuGlyArgLeuGlnSerValLeuThrLysAlaGluHisLeuSerLysLeuProAla 220
Db 1047 GTGTTCTCTCCCAACATGTCCTGAGGAGAGGAGGATATCTGACCTCGCTCAACCC 1106
Qy 221 AspThrProTyrSerGlnPheAlaTyrLysPheGlnGluTrpGlyLeuGluLysGlyTrp 240
Db 1107 GAGACCCGCTACTCCAGTTCGAGCACAGTTCAGGAGATCGGGCTCGAGCGGGGTGG 1166
Qy 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
Db 1167 GGTGACACCGCTGAGCGGCTCTCGAGATGATCAGCTCTGTTGGATCTCTTTGAGCT 1226
Qy 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIlePheAsnValVal 280
Db 1227 CCGGACCGGTGCACTCTCGAGAGTCTTGGATAGGGTTCCTCATGGTCTTCAAGTGTG 1286
Qy 281 ValValSerProHisGlyTyrPheGlyGlnAlaAsnValLeuGlyLeuProAspThrGly 300
Db 1287 ATCATGTCTCCCAAGTACTTGTCTGAGACGACGACGCTCTGTTTATCCGATACCGGT 1346
Qy 301 GlyGlnIleValTyrIleLeuAspGlnValArgAlaLeuGluAsnGluMetValLeuArg 320
Db 1347 GGCAGGTGTTGTTTACATCTCGATCAAGTTCGTGCTCGCTAGAGAAAGAAATGCTTCC 1406
Qy 321 LeuLysLysGlnGlyLeuAspValSerProLysIleLeuIleValThrArgLeuIlePro 340
Db 1407 ATTAAGCAACAGAGACTGGATATTTCTCTCGGATTTCTATTATCTCGCTCTTCCCA 1466
Qy 341 AspAlaLysGlyThrSerCysAsnGlnArgLeuGluArgIleSerGlyThrGlnHisThr 360
Db 1467 GACGCGGTTGGAAACCACTCTGCGCCAGCGCTTGGAGAAAGTCTTTGGACCGAGTACTCC 1526

QY 296 LeuProAspThrGlyGly----- 301
Db 3018 TACCCTGACACTGGCGTCAGGTACAGAGCTTAGTGATTACTATTTCCCTTAGGCTTTG 3077
QY 301 ----- 301
Db 3078 TTTGGGTATAGAGGATTGAAGTGAATTGAGGTGTATTAAAGAGGATTGAAGAAAAATT 3137
QY 301 ----- 301
Db 3138 AGTTTATATTACATTCAATACACCAATACACCACTCAATCCACTCAATTGAGATTAC 3197
QY 302 -----Gln11 303
Db 3198 CCMAACAAGCCCTTAGCTACTTTCCACTTCCAGTTTCTCTATTGGCATCGTTGAGGT 3257
QY 303 eValTyrlleLeuAspGlnValargAlaLeuGluAsnGluMetValLeuArgLeuLysly 323
Db 3258 TGTGTACATTCTGGATCAGGTCCGCTCTTGGAGAAATGAGATGCTTCTGAGGATTAAAGCA 3317
QY 323 sdGlyLeuAspValSerProLysIleLeulle----- 334
Db 3318 GCAGGCCCTTGATACCTCCGAAGATCCTCAT-TGTATGTTTGGAGCCACGTTTCACT 3376
QY 334 ----- 334
Db 3377 TCTGAATCCTTTTTTCACTGTGCTTGA-TTACTCAGTAAATGTGCTACATGATCTTA 3436
QY 335 -----ValThrArgLeulleProAspAlaLysGlyThrSerCysAsnSlnArgIle 351
Db 3437 TTTGTTGAGGTTTACAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3496
QY 351 uGluArgIleSerGlyThrGlnHisThrTyrlleLeuArgValProPheArgAsnGluAs 371
Db 3497 GAGGAGGTCATTGTTACTGAGCACACACATCATTCGGTTCCTTTCGAAATGAGAA 3556
QY 371 nGlyIleLysLysIleSerArgPheAspValTrpProTyrlleLeuGluThrPheAl 391
Db 3557 TGGCATCCTCCGCAAGTGGATCTCTGTTTGATGTCCTGGCCATACCTGGAGACATACAC 3616
QY 391 aglu----- 392
Db 3617 TCGAGTATACCGATTATCTGACTGGATGCTCTACACAGCATAGCATGTTTGAGTAATATAC 3676
QY 393 -----AspAlaalaGlyGluIleAlaalaGluLeuGlnG 404
Db 3677 TGAAGCCATGCATTCTGTCTGCAGGATGTTCCAGTGAATTAATGAAGAAATGAGGC 3736
QY 404 YThrProAspPheIleIleGlyAsnTyrlSerAspGlyAsnLeuValAlaSerLeuLeuSe 424
Db 3737 CAAGCCTGACCTTATCATTTGGCAACTACAGCGATGGCAACCTAGTCCCACTCTGCTGCG 3796
QY 424 rTyrlsMetGlyIleThr----- 430
Db 3797 GCACAAGTTGGAGTCACCTCAGTCTGTCTGTTGGTTTGTACATGATTTTGAGTATCT 3856
QY 431 -----GlnCysAs 433
Db 3857 TTAATAATATTAGTTATTATTCAATTGCTTAATGCTTTTGTACATCTTGCAGTGTAC 3916
QY 433 nIleAlaHsAlaLeuGluLysThrLysTyrlProAspSerAspIlePheTrpLysAsnPh 453
Db 3917 CATCGCTCATGCTTGGAGAAAACCAATACCCTCACTCGACATATACTTGCACAAATT 3976
QY 453 eAspGluLysTyrlHisPheSerCysGlnPheThrAlaAspIleAlaMetAsnAl 473
Db 3977 CGACGCCAGTACCACTTCTCTGGCAGTTTCACAGCTGACCTTAATTGCCATGAACACAC 4036
QY 473 aAspPheIleIleThrSerThrTyrlGlnGluIleAlaGly----- 486
Db 4037 CGATTTTCATCACCAGCACATTCGAAGAAATCGCGGAAGGTAGAAATTGTATATTAG 4096

QY 487 -----S 487
Db 4097 TAGCTGTGCTTTAGTAGTAATAAACTAGTATGTATGTATCTTTCTGTGTGTTCTGCA 4156
QY 487 erIysAsnThrValGlyGlnTyrlGluSerHisThrAlaPheThrLeuProGlyLeuTyra 507
Db 4157 GCAAGACACCGTGGGCGAGTACAGTCCACATCGGTTCACTTCTTCTGGGCTTACC 4216
QY 507 zGValValHsGlyIleAspValPheAspProLysPheAsnIleValSerProGlyAlaA 527
Db 4217 GTGTGTCATGTCATGTCATGTTTTCGATCCCAAGTTCACATTTGCTCCCTGGAGCAG 4276
QY 527 sPmetSerIleTyrlPheProHisThrGluLysAlaLysArgLeuThrSerLeuHisGlyS 547
Db 4277 ACATGAGTGTACTACCGGTATACGGAAACCCGACAGAGACTCACTGCCTTCCATCCTG 4336
QY 547 erIleGluAsnLeulleTyrlAspProGluGlnAsnAspGluHis----- 561
Db 4337 AAATCGAGGAGCTCATCTACAGCGAGTCCGAGAACTCCGAGCACAAAGTGAGTATACTGAA 4396
QY 561 ----- 561
Db 4397 AACTGTTCCATGTCTTACTGCGACCAATCAGCTTGTAAATCTCCACACCCCATGCGAT 4456
QY 562 -----IleGlyHisLeuAsp----- 566
Db 4457 GATCTATCCATCTTTCTATCTGTCACTGAG-CTGAACACCTGCTGTTTACTTGCATCCA 4515
QY 567 -----AspArgSerLysProIleLeuPheSerMetAlaArgLeuAspArgV 582
Db 4516 GGTTCGTGCTGAAGGACAAAGAACCGCATCATCTTCTGATGGCGCTCTCGACCGCG 4575
QY 582 alLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeuArgLuuLeuV 602
Db 4576 TGAAGAACATGACAGCCCTGCTGAGATGTACGGCAGAACCGCGCTCGAGGAGCTGG 4635
QY 602 aLasnLeuValValAlaGlyTyrlAsnAspValAsnLysSerLysAspArgLuuGluI 622
Db 4636 CGAACCTCGTGATGTTGCCGT---GACCACGGCAGGAGTCCNAGCAGAGGAGGAGC 4692
QY 622 leAlaGluIleGluLysMetHisGluLeulleLysThrHisAsnLeuPheGlyGlnPheA 642
Db 4693 AGCGGAGTTCAGAAGATGTACAGCTCTCATCGCAGTACAAGTTTGAAGGGCCATATCC 4752
QY 642 rGTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrlArgTyrlleAlaA 662
Db 4753 GGTGATCTCGCGCGCAGATGAACCGGTCCGCAACGGGAGCTGTACCGCTACATTTGCG 4812
QY 662 sPThrHisGlyAlaPheValGln----- 669
Db 4813 ATACGAAGGCGCGATTCTGTGAGGTATATGCACACACACACACTTGGATCTAATAT 4872
QY 669 ----- 669
Db 4873 CTAACTCCCAAGTTCCTCCACACGCTGCAATCTACTTTTCAGACACACACAGTCACCTGAAT 4932
QY 670 -----ProAlaLeuTyrlGluAlaPheGlyL 678
Db 4933 CATTTTCATCTTGTGTTTGTGTTGGTAGCTCGCTTCTACGAAGCGTTCCGCC 4992
QY 678 euthrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyP 698
Db 4993 TGACTGTGATCGAGTCCATGACGTGCGGTCTGCAACGATCGCGACTGCCATGGCGGCC 5052
QY 698 roAlaGluIleIleGluHisGlyValSerGlyPheHisIleAspProTyrlHisProGluG 718
Db 5053 CTGCTGAGATCATCTGCGAGCGGGTATCTGGCTGCACATTTGACCTTACACAGCGACA 5112
QY 718 lnaValAlaMetAlaAspPheAspArgCysLysGlnAspProAspHisTrpV 738
Db 5113 AGGCCCGGATATCTGTCACATTTCTTTGACAAATGCAAGGCGAGATCCGAGCTACTGGG 5172
QY 738 aLasnIleSerGlyAlaGlyLeuGlnArgIleTyrlGluLys----- 751

D _b	5173	ACAAGATCTCACAGGACGACCTCGAGAGAATTTATGAGAAATATGCAGTATTTTCTCTC	5232
Q _y	751	-----	751
D _b	5233	CTGCCATACAAATGTAAAACTCTTGTTGACTGAGGGCGCATCTGTTTACTCCCACGGACA	5292
Q _y	751	-----	751
D _b	5293	CTCGAAATCTGCCGTACCCCTTCTCTAGTTAGGAGAGTAGTAAAAAATACTGCACACTA	5352
Q _y	752	-----TyrThrTrpLysIleTyrSerGluArgLeuMetThrLeuA	765
D _b	5353	CAAGCTTTGGATTGCTCAGGTACACCTGGAAAGCTCTACTCCGAGAGGCTGATGACCTGA	5412
Q _y	765	IaGlyValTyrGlyPheTrpLysTyrValSerLysLeuGluArgLeuGluThrArgArgT	785
D _b	5413	CCGGCGTGTCACGGTCTTCGAGAGTACGTGAGACCACTGGAGAGCGCGAGACCGCGCCT	5472
Q _y	785	YrLeuGluMetPheTyrIleLeuLysPheArgGluLeu	797
D _b	5473	ACATCGAGATGTCTACGCCCTGAAGTACGTCAGCTG	5510

RESULT 4

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US-08-684-005-1
; Sequence 1, Application US/08684005
; Patent No. 6682918
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Buikema, William J.
; APPLICANT: Bauer, Christopher C.
; TITLE OF INVENTION: BACTERIAL SUCROSE SYNTHASE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,005
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARSB:508
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-684-005-1

Alignment Scores:
Pred. No.: 1 6e-201 Length: 2700
Score: 1833.00 Matches: 259
Percent Similarity: 66.33% Conservative: 163
Best Local Similarity: 45.62% Mismatches: 251
Query Match: 43.16% Indels: 14
DB: 4 Gaps: 7

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Query Match: 10.45% Indels: 164
DB: 1 Gaps: 24

US-10-080-114a-12 (1-809) x US-08-175-471-6 (1-3509)

241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
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532 GGAGACACCATCGCGAGCTT-----GCG 555

261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276
|||||
556 CCGGTTGAGACGACCAAGAGAGTTCACAGGAACTTCTCTGACCTTACCGCTGCTGCT 615

277 -----PheAsnValValValValSerProHisGlyTyrPhe----- 288

616 GACGACAAATAGGAGAGAGAGCTTACATGTCTCATCGCGTGCATCTTGTTCGT 675

289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
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676 GGAGAAACATGGAACTAGCTGATCTCATACAGTGGCCAGGTGAATATATGTGTC 735

308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysLysGlnGlyLeuAsp 327
:::
736 GAACCTTCAAGAGCG-----ATGTCA 756

328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
|||||
757 ATGATGCTGGAGTGTACAGGTGACCTTCTACTGCTCAAGTGTCAATCTCTGACGTG 816

342 -----AlaLysGlyThrSerCysAsnGlnArg 350
:::
817 GACTGGAGCTACGTGAGCCCAACCGAGATGTTATCGCGCGTTCATATGATGAGAGGG 876

351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
:::
877 ATGGGTGAGAGTGGCGA-----GCCATCATTTGTGGCATACCGTGT----- 918

371 AsnGlyIleLeuLysTyrIleSerArgPheAspValTyrProTyrLeuGluThrPhe 390
:::
919 ---GGCGCGGGATATATACCTCAAGAGGAGCGTTGTGGCTTACCTCCACAGAGTT 975

391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
:::
976 GTCGATGAGCGCTTGGCATATCTGAACATGTCACAGGCTCTGGGAGAGCAGTTGGA 1035

405 Thr-----ProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal 419
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1036 AATGGGAGCGCAGTACTGCTTACGTATATACGGCACTATGCGGATGCTGGAGATGT 1095

420 AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
:::
1096 GCTGCTCTCTTCTGGTGGCTGAATGTGCCATGTGCTCACTGGCCACTCACTTGGG 1155

440 LysThrLys-----TyrProAspSerAspIlePheTyrLysAsnPheAspGlu 455
:::
1156 AGGAACAAGCTGGACAACTGCTGAAGCAAGGCGCATGTCACAGGAGGAGATCGATCG 1215

456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe 475
:::
1216 ACATACAGATCATAGAGCGGTATCAGGGGTGAGGAGCTGGCCCTGGATGCTCAGAGCTT 1275

476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
:::
1276 GTATACAGACCAAGCAGGAGGATGAT-----GAGCATGG----- 1314

496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
:::
1315 -----GGATGTGAC-----GATGATTTGATGTCAAG 1341

515 -----PheAsp 516
:::
1342 CTTGAGAAAGTGTGAGGACCGGCGGAGGCGGGGTAGCTGCCATGCTGTATCATG 1401

QY 517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
|||||
DB 1402 CCTAGGATGGTGGTGAATTCCTCGGGAAGATTTTCAGCAATGTTGTAGTTCAI----- 1455

QY 537 LysAlaLysArgLeuThrSerLeuHisGlySerIleGlyAsnLeuIleTyrAspProGlu 556
|||||
DB 1456 -----GAAGACATTGATGGGATGGTGCAC 1479

QY 557 GlnAsnAspGluHisIleGly----- 563
|||||

DB 1480 GTCAAGATGATGATGTTGGTGGTGGAGGGTGCCTCACCAAGTCAATGCCCCCAATTCG 1539

QY 564 -----HisLeuAspAspArgSerLysProIleLeuPheSerMetAlaArg 578
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DB 1540 GCGAAGTGAATGCGTCTCTGACCAACCTCAAGCCGATGATCTCTGGCGTTATCAAGA 1599

QY 579 LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu 598
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DB 1600 CCAGACCCGAGAAGAACATCACTACCTCTCGTCAAGCGTTTGGAGAGTGTCTCCACTC 1659

QY 599 ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
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DB 1650 AGGGAACCTTGCAACCTTACTCTCATCGGTAAACAGAGATGATCGACGACATGTCT 1719

QY 619 ArgGluGluIleAlaGluIleGluLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
|||||

DB 1720 GCTGGCATGCGAGTCTCTCACACAGTCTGAAGCTGATTCAGACAGTATCATCTGTATC 1779

QY 639 GlyGlnPheArgTyrIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
|||||

DB 1780 GGAAGCGTGGCGTTC---CCTAAGCATCACAAATCAGGTGACGTCCCGAGATCATCGC 1836

QY 659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
|||||

DB 1837 CTCGCGGCAAAATGAAGGGGTCTTTCATCAACCTCTCTGTTGAGCGGTGTGCTCTC 1896

QY 679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
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DB 1897 ACCGTGATCGAGGCTGGCGACACGGACTCCGATGTCGTACCAAGATGGTGGTCCG 1956

QY 699 AlaGluIleIleGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
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DB 1957 GTCGACATTACAAATGCAATTAACAACGAGCTGCTCGTTGATCCACACGACGAG 2010

QY 719 AlaValAsnLeuMetAlaAspPheAspArgCysLysGlnAspProAspHisTyrVal 738
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DB 2011 -----AACGCAATGCTGATGCACTGCTGAAGCTTGTGGCAGACAGAACCTGTGGCAG 2064

QY 739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTyrLysIleTyrSer 758
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DB 2065 GAATGCGGAGAAACGGCTGCGCAATCCAC---CTCTACTATGCGCGGAGCACTGC 2121

QY 759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTyrLysTyrValSerLysLeu 777
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DB 2122 GGCATCTACCTCACCGGTGGCGGGTGC----- 2151

QY 778 GluArgLeuGluThrArgArgTyrLeuGlu 787
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DB 2152 ---CGTTAAGGAACCGAGGTGGCTGAAG 2178

RESULT 6
US-08-718-777-6
; Sequence 6, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Woelker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: PHOSPHATE
; TITLE OF INVENTION: SYNTHASE IN PLANTS

; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Barbara Rae-Venter
 ; STREET: 260 Sheridan Avenue, Suite 440
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: JS/08/718,777
 ; FILING DATE: NOT YET ASSIGNED
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JS 08/175,471
 ; FILING DATE: 27-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara Rae-Venter
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.072.02US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)328-4400
 ; TELEFAX: (415)328-4477
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3509 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 112..3315
 ; US-08-718-777-6
 ;
 ; Alignment Scores:
 ; Pred. No.: 1,84e-40 Length: 3509
 ; Score: 444.00 Matches: 159
 ; Percent Similarity: 40.48% Conservative: 96
 ; Best Local Similarity: 25.24% Mismatches: 211
 ; Query Match: 10.45% Indels: 164
 ; DB: 2 Gaps: 24
 ;
 ; US-10-080-114A-12 (1-809) x US-08-718-777-6 (1-3509)
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 QY 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
 DB 532 GGAGACACCATCGCGAGCTT-----GCG 555
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 QY 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetile----- 276
 DB 556 CCGGTTGACAGCACCAGGAAGATTCCAGAGAACTTCTCTGACCTTACCGCTCGTCT 615
 QY 277 -----PheAsnValValValValSerProHisGlyTyrPhe--- 288
 DB 616 GACGACAATAAGGAGAAGCTTTACATTGTCTCATCGCGTGCATGCTTTGTCGT 675
 QY 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
 DB 676 GGAGAAACATGGAACCTAGTCTGTGATTCTGATACAGGTGGCCAGGTGAATATGTGTC 735
 QY 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysLysGlnGlyLeuAsp 327
 DB 736 GAACTTGCAAGAGCG-----ATGTCA 756
 QY 328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
 DB 757 ATGATGCTGGAGTGATACAGGGTGGACCTCTTCACTCGTCAAGTGTTCATCTCCTGACGTG 816

QY 342 -----AlaLysGlyThrSerCysAsnGlnArg 350
 DB 817 GACTGGAGCTACGGTGAGCCAAACCGAGATGTATGCGCGGTTCCTCAATGATGAGAGGGG 876
 QY 351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
 DB 877 ATGGGTGAGAGTGGCGGA-----GCTACATTGTGGCATACCGTCT----- 918
 QY 371 AsnGlyIleLeuLysLysTrpIleSerArgPheAspValTrpProTyrLeuGluThrPhe 390
 DB 919 --GGCCCGCGGATAAATACCTCAAGAAGAACGCTTGTGGCTTTACCTCCCAAGAGTTT 975
 QY 391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
 DB 976 GTCGATGGAGCCCTTGGCGATATCTGAACATGTCACAGGCTCTGGAGAGCAGGTGGGA 1035
 QY 405 Thr-----ProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal 419
 DB 1036 AATGGAGGCGCAGTACTGCTTACGTGATACATGGGCACCTATCCGATGCTGGAGATGT 1095
 QY 420 AlaSerLeuLeuSerTyrIysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
 DB 1096 GCTGCTCTCTTCTGCTGCTGCTGAATGTGCCAATGCTGCTGCTGCTGCTGCTGCTGCT 1155
 QY 440 LysThrLys-----TyrProAspSerAspIlePheTrpLysAsnPheAspGlu 455
 DB 1156 AGGAACAACCTGGACAACTGCTGAAGCAGGCGCATGCTCAAGGAGGAGATCGATCG 1215
 QY 456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAlaAspPhe 475
 DB 1216 ACATACAGATCATGAGGCGTATCGAGGGTGAGGAGCTGGCCCTGGATGCTCAGAGCTT 1275
 QY 476 IleIleThrSerThrTyrGlnGluIleAlaGlySerIysAsnThrValGlyGlnTyrGlu 495
 DB 1276 GTAATCACGAGCACAGGAGGAGATTGAT-----GAGCAGTGG--- 1314
 QY 496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
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 QY 515 -----PheAsp 516
 DB 1342 CTTGACAAAAGTGTGAGGCGCACGCGCGCGGTAGCTGCCATGCTGCTTACATG 1401
 QY 517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
 DB 1402 CCTAGGATGGTGGTGAATCTCTCGGGAATGGATTTCGCAATGTTGTAGTTCTAT--- 1455
 QY 537 LysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu 556
 DB 1456 -----GAACACATTGATGGGATGGTGAC 1479
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 DB 1480 GTCAAAAGATGATATCGTTGTTGGAGGGTGCCTCACCAAGTCAATGCCCCCAATTGG 1539
 QY 564 -----HisLeuAspAspArgSerLysProIleLeuPheSerMetAlaArg 578
 DB 1540 GCGAAGTATGCGGTCTCTGACCAACCTTCACAGCCCGATGATCTGGCGTTATCAAGA 1599
 QY 579 LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu 598
 DB 1600 CCAGACCCGAGAGAGACATCACTACCTCGTCAAGCCCTTTGGAGAGTGTCTGCCATCT 1659
 QY 599 ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
 DB 1660 AGGGAACCTTGCAAACCTTACTCTGTATCATGGGTATACAGAGATCATCGACGATGTCT 1719
 QY 619 ArgGluGluIleAlaGluLeuGluLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
 DB 1720 GCTGGCAATGCCAGTGTCTCTCACCAAGTCTTCAAGCTGATTGACAGTATGATCTGATC 1779
 QY 639 GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658

Db 1780 GSAAGCGTGGGTTTC---CCTAAGCATCACAACTCAGGCTGCGTCCCGAGATCTATCGC 1836
Qy TyrLealaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
Db 1837 CTGCGCGCAAAATGAAGGGCTTTCATCAACCTCTCTCTGTTGAGCGGTTGGTCTC 1896
Qy ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
Db 1897 ACCGTGATCGAGGCTGGCGCACAGGACTCCGATAGTCGCTACCAAGATGGTGTCTCG 1956
Qy AlaGluLeuLeuGluHisGlyValSerGlyPheHisLeuAspProTyrHisProGluGln 718
Db 1957 GTGACATTAACAATGCAATTAACAACAGGACTGCTCTGTGACCCACAGCAGCAG--- 2010
Qy AlaValAsnLeuMetAlaAspPhePheAspArgCysLysGlnAspProAspHisTyrVal 738
Db 2011 -----AACGCCATCGCTGATCGACTGCTGCTGCTGGCGAGCAAGAACCTGTGGCAG 2064
Qy AsnLeuSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTyrLysIleTyrSer 758
Db 2065 GAATCGCGGAGAAACGGGCTGGCAACATCCAC---CTTACTCATGGCGGAGCACTGC 2121
Qy GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTyrPheTyrValSerLysLeu 777
Db 2122 CGCACTTACCTCACCAAGGCTGGCGGCTGC----- 2151
Qy GluArgLeuGluThrArgArgTyrLeuGlu 787
Db 2152 ---CGGTTAGGAACCCGAGGTGGCTGAAG 2178

RESULT 7

US-09-078-862-2
; Sequence 2, Application US/09078862
; Patent No. 6091003

GENERAL INFORMATION:

; APPLICANT: Nan, Guo-Ling
; APPLICANT: Nagai, Chifumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
; TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/078,862
; FILING DATE: 14-MAY-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: US-03321
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-09-078-862-2

Alignment Scores:

Pred. No.: 1-84e-40 Length: 3509
Score: 444.00 Matches: 139
Percent Similarity: 40.48% Conservative: 96
Best Local Similarity: 25.24% Mismatches: 211
Query Match: 10.45% Indels: 164
DB: 3 Gaps: 24

US-10-080-114A-12 (1-809) x US-09-078-862-2 (1-3509)

Qy 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
Db 532 GAGACACCATCGCGAGCTT----- 555
Qy 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276
Db 556 CCGGTTGAGACACCAAGAAAGAGTTCAGAGAACTTCTTGACCTTACCGTCTGGTCT 615
Qy 277 -----PheAsnValValValSerProHisGlyTyrPhe--- 288
Db 616 GACGACAATAAGGAGAGAGCTTTACATTGTGCTCATCAGCGTGCATGCTGTTCGT 675
Qy 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
Db 676 GGAGAAAACATGGAACCTAGTCTGATTCTGATACAGGTGGCCAGGTGAATATATGTGTC 735
Qy 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysGlnGlyLeuAsp 327
Db 736 GAACTTGCAAGAGCG-----ATGTCA 756
Qy 328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
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Qy 342 -----AlaLysGlyThrSerCysAsnGlnArg 350
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Db 919 ---GGCGCGCGGATATAATACCTCAAGAGAGAGCGGTGCTGGCTTACCTCCAGAGTTT 975
Qy 391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
Db 976 GTCGATGGAGCCCTTTCGCGCATATCTGAACATGTCGAAGGCTCTGGGAGAGGTTGGA 1035
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Qy 456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAlaAspPhe 475
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Db 1276 GTAATCAGAGCAACAGGAGGAGATTGAT-----GAGCAGTGG--- 1314
Qy 496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValHisGlyIleAspVal--- 514
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QY 579 LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu 598
Db 1600 CCAGACCCGAGAGAACATCATCTACCTCGTCAAGCGTTTGAGAGTCTCGTCCACTC 1659
QY 599 ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
Db 1660 AGGAATCTGCAACCTTACTGATGATGGTTACAGAGATGATGATGATGATGATGATG 1719
QY 619 ArgGluLeuAlaGluIleGluLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
Db 1720 GCTGGCAATGCCAGTGTCTCCACACACAGTCTGAAGCTGATGACAAAGTATGATCTG 1779
QY 639 GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
Db 1780 GGAAGCGTGGCGTTC-----CCTAAGCATCATCAATCAGCTCCCGAGATCTATCCG 1836
QY 659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
Db 1837 CTCGGCCCAAAATGAAGGGCGTCTTCATCACTGCTCTCTGTTGAGCGTTGCTC 1896
QY 679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
Db 1897 ACCCTGATCGAGCTGGCGCACACGAGTCTCCGATAGTCCGATGATGATGATGATG 1956
QY 699 AlaGluIleLeuGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
Db 1957 GTCGACATTAACAATGATTAACAACAGGACTGCTGTTGACCCACACAGCCAG-----2010
QY 719 AlaValAsnLeuMetAlaAspPhePheAspArgCysLysGlnAspProAspHisTrpVal 738
Db 2011 -----ACGCCATCGTGTGACTGCTGAAGCTTGTGGCAGACAGAACCTGTGGCAG 2064
QY 739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTrpLysIleTyrSer 758
Db 2065 GAATGCGGAGAAACGGCTCGGCAATCCAC---CTCTACTCATGCGCGGAGCACTGC 2121
QY 759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTrpLysTyrValSerLysLeu 777
Db 2122 CGCACTTACCTCACAGGGTGGCGGGTGC-----2151
QY 778 GluArgLeuGluThrArgArgTyrLeuGlu 787
Db 2152 ---CGGTTAGGAACCCGAGTGGCTGAAG 2178
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RESULT 8

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US-09-051-341-6
; Sequence 6, Application US/09251341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shemmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
```

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NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter, Ph.D.,
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURES:
NAME/KEY: CDS
LOCATION: 112..3315
US-09-051-341-6
Alignment Scores:
Pred. No.: 1,84e-40 Length: 3509
Score: 444.00 Matches: 159
Percent Similarity: 40.48% Conservative: 96
Best Local Similarity: 25.24% Mismatches: 211
Query Match: 10.45% Indels: 164
DB: 3 Gaps: 24
US-10-080-114a-12 (1-809) x US-09-051-341-6 (1-3509)
QY 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleGlnAla 260
Db 532 GGAGACACCATCGCGAGCTT-----GCG 555
QY 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle-----276
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QY 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
Db 676 GGAGAAAACATCGGAACCTAGTCTGCGTATCTGATACAGTGGCCAGGTGAAATATGTCGTC 735
QY 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysGlnGlyLeuAsp 327
Db 736 GAACTTCAAGAGCG-----ATGTCA 756
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QY	328	ValSerPro	-----LysIleLeuIleValThrArgLeuIle	-----ProAsp	--- 341
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QY	342	-----	AlaLysGlyThrSerCysAsnGlnArg	350	
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Db	817	GACTGGAGCTACGGTGTAGCCAAACCGAGATGTT	TATGCGCGCGTTCCTCAATGATGAGAGAGG	876	
QY	351	LeuGluArgIleSerGlyThrGlnHisThrTy	rIleLeuArgValProPheArgAsnGlu	370	
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Db	877	ATGGTGAGAGTGGCGA	-----GCCCTCATTTGTGGCGATACCGTGT	918	
QY	371	AsnGlyIleLeuLysTyrIleSerArgPheAsp	ValTyrProTyrIleuGluThrPhe	390	
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Db	919	--GGGCGCGGATAAATACCTCAAGAAGAGCG	TGTGGCTTACCTCCAAAGAGTTT	975	
QY	391	AlaGluAspAlaAlaGlyGluIle	-----AlaIaGlnLeuGlnGly	404	
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QY	420	AlaSerLeuLeuSerTyrLysMetGlyIleThr	GlnCysAsnIleAlaHisAlaLeuGlu	439	
Db	1096	GCTGCTCTCTTCTGTGTGCGCTGAATGTCCA	ATGTGCTCACTGCCCACTCACTTGG	1155	
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QY	456	LysTyrHisPheSerCysGlnPheThrAla	AspIleIleAlaMetAsnAsnAlaAspPhe	475	
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QY	476	IleIleTrSerThrTyrGlnGluIleAla	aglySerLysAsnThrValGlyGlnTyrGlu	495	
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QY	496	SerHisThrAlaPheThrLeuProGlyLeu	TyrArgValValHisGlyIleAspVal	514	
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QY	515	-----	-----PheAsp	516	
Db	1342	CTTGAGAAAGTGTGAGGGCAGGGCAGGGG	GTGAGGGGTTAGCTGCCATGTCTTACATG	1401	
QY	517	ProLysPheAsnIleValSerProGlyVala	AspMetSerIleTyrPheProHisThrGlu	536	
Db	1402	CCTAGGATGTTGGTATCTCTCCGGGATGGA	TTCAGCAATCTGTAGTTTCAT	1455	
QY	537	LysAlaLysArgLeuThrSerLeuHisGly	SerIleGluAsnLeuIleTyrAspProGlu	556	
Db	1456	-----	-----GAGACATTTGATGGGATGGTGAC	1479	
QY	557	GlnAsnAspGluHisIleGly	-----	563	
Db	1480	GTCAAAAGATATATCGTTGTGTTGGAGGG	TGCCTCACCCCAAGTCAATGCCCCCAATTGG	1539	
QY	564	-----HisLeuAspAspAspSerLysPro	IleLeuPheSerMetAlaArg	578	
Db	1540	GCCGAGTGTATCGGTCCTGACCAACCTCA	CAGCCGATGATCTCGGGGTATCAAGA	1599	
QY	579	LeuAspArgValLysAsnIleThrGlyLeu	ValGluAlaPheAlaLysCysAlaLysLeu	598	
Db	1600	CCAGACCCGAAGAAGACATCACTACCTGT	CAAGACCTTTGGAGAGTGTCTGCCACTC	1659	
QY	599	ArgGluLeuValAsnLeuValValAlaGly	TyrAsnAspValIleLysSerLysAsp	618	
Db	1660	AGGGAACTTGCAAACCTTACTCTGTATG	ATGGGTAAACAGAGATGACATCGACGACATGTCT	1719	

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619 ArgGluGluIleAlaGluIleGlyLysMetHisGluLeuLeuIleLysThrHisAsnLeuPhe 638
1720 GCTGGCAATGCCAGTGTCTTCACACACAGTTCTGAAGCTTGATTGCACAAGTATGATCTGTAC 1779
QY GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
1780 GGAAGCGTGGGTTC-----CCTAAGCATCAAAATCAGGCTCACGTCCTCGTTGAGCGGTGGTCTC 1836
QY TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
1837 CTCGGCCCAAATAAGAGGGCGTCTTCATCAACCCTGCTCTCGTTGAGCGGTGGTCTC 1896
QY ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
1897 ACCCTGATCAGGCTGGCGCACACGGACTCCGAGTCTCCGATAGTCGCTACCAAGAATGGTGGTCCG 1956
QY AlaGluIleLeuHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
1957 GTGACGATTACAATGATTAACACAGGACTGCTGCTGTTGACCCACACAGCCAG----- 2018
QY AlaValAsnLeuMetalAspPheAspArgCysLysGlnAspProAspHisTrpVal 738
2011 -----AACGCCATCGTGTGATCGACTCTGAAGCTTGTGGCAGACAGACCTGTGSCAG 2064
QY AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGlnLysTyrThrTrpLysIleTyrSer 758
2065 GAATGCCGAGAAAACGGGCTGGCAACATCCAC---CTCTACTCATGGCCGAGCACTGC 2121
QY GluArgLeuMetThr--LeuAlaGlyValTyrGlyPheTrpLysTyrValSerLysLeu 777
2122 CGCACTTACCTCACACGGGTGGCGGGTGC----- 2151
QY GluArgLeuGluThrArgArgTyrLeuGlu 787
2152 ---CGTTAAGARACCCGAGGTGCTGAAG 2178

RESULT 9
US-09-866-153-12
; Sequence 12, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Zea mays
US-09-865-153-12

Alignment Scores:
Pred. No.: Length: 3509
Score: 1.84e-40
Percent Similarity: 444.00 Matches: 159
Best Local Similarity: 40.48% Conservative: 96
Query Match: 25.24% Mismatches: 211
DB: 10.45% Indels: 164
      4 Gaps: 24

US-10-080-114A-12 (1-809) x US-09-866-153-12 (1-3509)

QY 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuAspIleIleGlnAla 260
Db 532 GGAGACCACTCGCGAGCTT----- 555
QY 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276

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Db 556 CCGGTTGAGACGACCAAGAAAGTTCCAGAGGAACCTTCTCTGACCTTACCGTCTGGTCT 615
Qy 277 -----PheAsnValValValSerProHisGlyTyrPhe--- 288
Db 616 GACGACAAAGGAGAGAGCTTACATGTGCTCATCAGCGTGCATGTCTTGTCTG 675
Qy 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
Db 676 GCGAAGAAACATGAACTAGTCTGTGATTCGATACAGGTGCGCCAGGTGGAATAATGTGTC 735
Qy 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysLysGlnGlyLeuAsp 327
Db 736 GAATCTGCAAGACG-----ATGTCA 756
Qy 328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
Db 757 ATGATCGCTGGAGTGTACAGGTGGACCTTCTCCTGCTCAAGTGTCTCTCTGAGTGG 816
Qy 342 -----AlaLysGlyThrSerCysAsnGlnArg 350
Db 817 GACTGGAGCTACGGTGAGCCAAACGAGATGTTATGCGCCGGTTCMAATGATGGAGGGG 876
Qy 351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
Db 877 ATGGGTGAGAGTGGCGGA-----GCCTACATTGTGCGTACCGTGT----- 918
Qy 371 AsnGlyIleLeuLysLysTrpIleSerArgPheAspValTrpProTyrLeuGluThrPhe 390
Db 919 ---GGCCCGCGGATAAATACTCMAGAGGAGCGTGTGGCTTACTCTCCAGAGTTT 975
Qy 391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
Db 976 GTGATGGAAGCCCTTGGCATATCTCTGAACATGTCCAAAGGCTCTGGGAGAGCGAGTTGGA 1035
Qy 405 Thr-----ProAspPheIleIleGlyAsnTrpSerAspGlyAsnLeuVal 419
Db 1036 AATGGAGGCGCAGTACTGCTTACGTGATATACATGGGCACCTATGCGGATCTGGAGATGT 1095
Qy 420 AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
Db 1096 GCTGCTCTCTTCTTCTGGTGGCGTGAATGTCCCAATGTGTCTCAGTGCCTACTCTGGG 1155
Qy 440 LysThrLys-----TyrProAspSerAspIlePheTrpLysAsnPheAspGlu 455
Db 1156 AGGAACAAGCTGGAACAACACTGCTGAAGCAAGGCGCATGTCCAGAGGAGAGATCGATTGC 1215
Qy 456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe 475
Db 1216 ACATCAAGATCATAGAGGCGGTATCGAGGGTGAGAGCTGCGCCCTGGATGCGTCAGAGCTT 1275
Qy 476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
Db 1276 GTAAATCAGGACACAGGCGAGAGATTGAT-----GAGCAGTGG--- 1314
Qy 496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
Db 1315 -----GATGATTTGATGTCAAG 1341
Qy 515 -----PheAsp 516
Db 1342 CTTGAGAAAGTGTAGGCGCAGCGCGGGGTAGTCCCATGCTCGTATCATG 1401
Qy 517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
Db 1402 CCTAGGATGGTGTGATTCTCTCCGGGAATGATTTCCAGCAATGTGTAGTTCAT----- 1455
Qy 537 LysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu 556
Db 1456 -----GAAGACATTGATGGGATGGTGAC 1479
Qy 557 GlnAsnAspGluHisIleGly----- 563
Db 1480 GTCAAGATGATATCGTGTGTTGGAGGTGCCTCACCCCAAGTCAATGCCCCCAATTGG 1539

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Qy 564 -----HisLeuAspArgSerLysProIleLeuPheSerMetAlaArg 578
Db 1540 GCGGAAGTGTATGGTTCCTGACCAACCCCTCACAGCCGATGATCTCGCGGTATATCAAGA 1599
Qy 579 LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu 598
Db 1600 CCGAACCCGGAAGAGACATCATCTACCTCGTCAAAGCGTTTGGAGAGTGTCTGCCACTC 1659
Qy 599 ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
Db 1660 AGGAACCTTCCAAACCTTACTCTGATCATGGTGAACAGATGACATCGACGACATGTCT 1719
Qy 619 ArgGluGluIleAlaGluIleGlyLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
Db 1720 GCTGGCAATGCCAGTGTCTCACACAGCTTCTGAAGCTGATTGACAAAGTATGATCTGAC 1779
Qy 639 GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
Db 1780 GGAAGCGTGGCGTTC---CCTAAGCATCAACAATCAGGCTGACGTCCTCCGGAGATCTATCG 1836
Qy 659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
Db 1837 CTGCGGCCAAATGAAGGCGTCTTCTCAACCTGCTCTCGTTGAGCCGTTGGTCTC 1896
Qy 679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
Db 1897 ACCTGATCGAGGCTGCGGCACACGGACTCCCGATAGCTGCTACCAAGAATGGTGTCCG 1956
Qy 699 AlaGluIleLeuHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
Db 1957 GTGACATTTCAAAATGCAATTAACAACAGGACTGCTGTTGACCCACACAGCCAG--- 2010
Qy 719 AlaValAsnLeuMetAlaAspPhePheAspArgCysLysGlnAspProAspHisTrpVal 738
Db 2011 -----AACCCATCGCTGATGACTGCTGAAGCTTGTGGCAGACAGAACCTGTGGCAG 2064
Qy 739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTrpLysIleTyrSer 758
Db 2065 GAATGCGGAGAAACGGGCTGCGCAACATCCAC---CTCTACTCATGCGCGAGCACTGC 2121
Qy 759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheThrLysTyrValSerLysLeu 777
Db 2122 CGCACTTACCTACCCAGGGTGGCGGGTGC----- 2152
Qy 778 GluArgLeuGluThrArgArgTyrLeuGlu 787
Db 2152 ---CGTTAAGGACCCGAGGTGGCTGAAG 2178

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RESULT 10

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US-09-693-467A-12
; Sequence 12, Application US/09693467A
; Patent No. 6686513
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-04331
; CURRENT APPLICATION NUMBER: US/09/693,467A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Zea mays
US-09-693-467A-12

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Alignment Scores: 1.84e-40 Length: 3509
Pred. No.: 444.00 Matches: 159
Score:

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STREET: 1130 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/C8/356,354
 FILING DATE: 20-DEC-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US PCT/EP93/01605
 FILING DATE: 22-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P42 20 758.4
 FILING DATE: 24-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Weilman, Edward A.
 REGISTRATION NUMBER: 24,735
 REFERENCE/DOCKET NUMBER: P/951-105
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 382-0700
 TELEFAX: (212) 382-0888
 TELEX: 236925
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3625 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Solanum tuberosum
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 121..3282
 OTHER INFORMATION: /note= "Sucrose-Phosphate-Synthase"
 US-08-356-354-3

QY		137	PheGluProPheAsnValSerValProArgProAsnArgSerSerIleGlyAsnGly	156
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QY		157	ValGlnPheLeuAsnArgHisLeuSerSerIleMetPheArgAsnArgAspCysLeuGlu	176
			:::::	
Db		130	AACGATTGGATTACAGTTAC-----TTAGAG	156
QY		177	ProLeuLeuAspPheLeuArgGlyHisArgHisLysGlyHisValMetMetLeuAsnAsp	196
			:::	
Db		157	GCGATACTGGATGTGTGGACCAGGCGTAGATCATAGAAGTCATCGTTCTGTGTGAGAAA	216
QY		197	ArgIleGlnSerLeuGlyArg-----LeuGlnSerValLeuThr	209
Db		217	AGA-----GGAGGTTTAGTCCGACGAGGTACTTGTGTGAGGAAGTTATTACT	264
QY		210	LysAlaGluGlu-----HisLeuSerLysLeuProAla-----	220
Db		265	GGATTCCGACTGAGACTGATTGGATCGTGCG--GGATCCGAGACAAGTA CTCCGAGTCCG	324

Db 1317 TGAT---CCATATTAGCGGTAACTGACGATCAAGCGCATGTCAGCTGTTA 1373
QY 512 eAspValPheAspProlysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPh 532
Db 1374 TGCAGGTTTATGCTGCTGATGCTGTAATCTCTCTGGATGGATGCCACATATTGT 1433
QY 532 eProHisThrGluLysAlaLysArgLeuSerLeuHisGlySerIleGluAsnLeuI 552
Db 1434 GCCACHTGAAGGTGACHTGATGTGTGAACN-----GAAGAAAGTGAAGTGGAGAC 1487
QY 552 eTyrAspProGluGlnAsnAspGluHisIleGlyHisLeuAspAspArgSerIleProI 572
Db 1488 CCCGATCCACTATTGGGCAGAGATTATGCGCTCTCTTTCTAATCAAGGAAGCTAT 1547
QY 572 eLeuPheSerMetAlaArgLeuAspArgValLysAsnIleThrGlyLeuValGluAlaPh 592
Db 1548 GATACATGCACTTCTGCTAGGCTGATCCCAAGAACCTCACTACTTTAGTGAAGCAAT 1607
QY 592 eAlaLysCysAlaLysLeuArgGluLeuValAsnLeuValValAlaGlyTyrAsnAs 612
Db 1608 TGGTGAATGTCGTCATGAGAGCTTGTAATCTTACTTTGATAATGGTAATCCAGA 1667
QY 612 pValAsnLysSerIysAspArgGluGluIleAlaGluIleGluLysMetHisGluLeuI 632
Db 1668 TAATATCGAGAAATGCTAGCACAATCTCGCACTTCTCTTCAATCTTGAAAATGAT 1727
QY 632 eLysThrHisAsnLeuPheGlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaAr 652
Db 1728 AGATAAGTATGATCTTATGCTCAAGAGCTTGTAATCTTACTTTGATAATGGTAATCCAGA 1784
QY 652 gAsnGlyGluLeuTyrArgTyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLe 672
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QY 672 uTyrGluAlaPheGlyLeuThrValValGluAlaMetThrCysGlyLeuProThrPheAl 692
Db 1845 TATTGAGCTTTTGGACTGCTTGTGAGGACAGCTATGCTCTCCCAATGGTAGC 1904
QY 692 aThrLeuHisGlyGlyProAlaGluIleGluHisGlyVal-----SerGlyPheHi 710
Db 1905 CACAAAAATGGAGACCTCTTGATATA-----CATAGGTTCTTGACAAATGCTCTT 1958
QY 710 sIleAspProTyrHisProGluGlnAlaValAsnLeuMetAlaAspPheAspArgCy 730
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QY 730 sLysGlnAspProAspHisTrpValAsnIleSerGlyAlaGlyLeuGlnArgIleTyrGl 750
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QY 750 uLysTyrThrTrp-----LysIleTyrSerGluArgLeu 761
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RESULT 12

US-08-778-656-3
Sequence No. Application US/08778656
Patent No. 5976869
GENERAL INFORMATION:
APPLICANT: SONNEWALD, Uwe
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-3403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778.656
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,354
FILING DATE: 20-DEC-1994
APPLICATION NUMBER: US PCT/EP93/01605
FILING DATE: 22-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P42 20 758.4
FILING DATE: 24-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Solanum tuberosum
FEATURES:
NAME/KEY: CDS
LOCATION: 121..3282
OTHER INFORMATION: /note= "Sucrose-Phosphate-Synthase"
US-08-778-656-3
Alignment Scores:
Pred. No.: 3,79e-40 Length: 3625
Score: 441.50 Matches: 183
Percent Similarity: 40.76% Conservative: 117
Best Local Similarity: 24.86% Mismatches: 270
Query Match: 10.40% Indels: 167
DB: 2 Gaps: 31
US-10-080-114A-12 (1-809) x US-08-778-656-3 (1-3625)
QY 137 PheGluProPheAsnValSerValProArgProAsnArgSerSerIleGlyAsnGly 156
Db 70 TTCTACTCCGTTAATCTCTCTAGCACACGCGGAGAGCTGCGCGGAGAGATGCGGGA 129
QY 157 ValGlnPheLeuAsnArgHisLeuSerSerIleMetPheArgAsnArgAspCysLeuGlu 176
Db 130 AACGATTGGATTACAGTTAC-----TTAGAG 156
QY 177 ProLeuLeuAspPheLeuArgGlyHisArgHisIysGlyHisValMetMetLeuAsnAsp 196
Db 157 GCGATTCGATGTTGGACCGACGAGGCTAGATAGATAAGAAAGTCATCGTTGTTTGGAGAA 216
QY 197 ArgIleGlnSerLeuGlyArg-----LeuGlnSerValLeuThr 209
Db 217 AGA-----GGAGGTTTAGTCCGACGAGGTACTTTGTTGAGGAAGTTATTACT 264
QY 210 LysAlaGluGlu-----HisLeuSerIysLeuProAla----- 220
Db 265 GGATTCGATGAGACTGATTTCATCGTTGCTGGATCCGAGCACACAGCTACTCGGAGTCCG 324
QY 221 -----AspThrProTyrSerGlnPheAlaTyrLys-PheGlnGluTyrGlyLeuGl 237
Db 325 CAGAGAAAGGAATACTAGGCTCGAGAATATGTGTCGAGGAGATTTCGAAATTTGGCTGCCAG 384
QY 237 uLys-----GlyTyrGlyAspThrAlaGlyHisValLe 248

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Db 385 AAAAAGCAGCTTCAGGAGGAGCAAGCTCAGTGCATGGAACACGCCGCTCAAGCAAGCTGAA 444
Qy 248 gduMet----- 250
Db 445 AGAGGTCGCGAGAGAGCAGCTGCTGATATGTCAGAGGATCTATCTGAGGAGAGAAAGGA 504
Qy 251 -----IleHisLeuLeuAspIlelleGlnAlaProAspProSerTh 265
Db 505 GATATAGTCGCTGACATGCTATCTCAG-----GTGAAAGTACAGAGGCCGATG 555
Qy 265 rLeuGluLysPheLeu-----GlyArgIleProMetII 276
Db 556 CCTAGATCAGTCTCTGTGAGACAATGGAAGCATGGGTGCTAGTCAGCAGAGAGAAAGAG 615
Qy 276 ePheAsnValValValSerProHisGlyTyrPhe---GlyGlnAlaAsnValLeuGI 295
Db 616 CTTTAT-ATCGTCTTAAAGTTTACATGTTTAAATTCGGGGTGAGAAATATGAGGCTTG 674
Qy 295 yLeu---ProAspThrGlyGlyGlnIleValTyrIleLeuAspGlnValArgAlaLeuGI 314
Db 675 ACGGATTCGTATCTGCTGCTGAGTGAAGTATGTTGTAATTCGAGAGGCCCTTAGG 734
Qy 314 uAsn-----GluMetValLeuArgLeuLysLysGlnGlyLeuAs 327
Db 735 GTCGATGCCAGGTGTATATCGGGTGTGACTTGCTTACTAGACAAGTATCT----- 783
Qy 327 pValSerProLysIle-----LeuIleValThrArgLeuII 339
Db 784 ---TCACCAAGATGATGAGCTATGCTGAGCCGACAGAGATGCTGAGCCCAATAG 839
Qy 339 eProAspAlaLysGlyThrSerCysAsnGlnArgLeuGluArgIleSerGlyThrGlnHI 359
Db 840 TACAGACGGCTGATGACTGAGATGCGGAG-----AGTAGTCG 878
Qy 359 sThrIleLeuArgValProPheArgAsnGluAsnGlyIleLeuLysLysTrpIleSe 379
Db 879 TGCTTATATTTCGCATCTCTTT-----GGACCAAGAGAGAAATATATTC 926
Qy 379 rArgPheAspValTyrProTyrLeuGluThrPheAlaGluAsAla----- 394
Db 927 AAAAGACAGCTATGCGCTTATATCCGAATTTGTTGTTGCTTAAACCATATAT 986
Qy 395 ---AlaGlyGluIleAlaAlaGluLeuGlnGlyThr-----ProAspPh 408
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Qy 408 eIlelleGlyAsnTyrSerAspGlyAsnLeuValAlaSerLeuLeuSerTyrLysMetGI 428
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Db 1107 TGTAACCAAGCTTTTCACTGCTCAGTCTCAGTCTGATGAGATAGTTGGACCACTGTGGC 1166
Qy 444 -----ProAspSerAspIlePheTrpLysAsnPheAspGluLysTyrHisPheSe 460
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Qy 460 rCysGlnPheThrAlaAspIlelleAlaMetAsnAlaAspPheIlelleThrSerTh 480
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Qy 480 rTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGluSerHisThrAlaPh 500
Db 1275 AAGACAGAGATGAC-----GAGCAATGGGCTTGTATGATGGGT 1316
Qy 500 eThrLeuProGlyLeuTyrArgValValHisGly-----II 512
Db 1317 TGAT---CCATATTAGAGCGTAAGTTACGTGCGAGGATCAAGCGCAATGTCAGCTGTA 1373
Qy 512 eAspValPheAspProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPh 532
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Db 1374 TGCAGGTTTATGCTCGTATGCTGTAAATTCTCTCTGGGATGGAGTTCCACCATATTGT 1433
Qy 532 eProHisThrGluLysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuII 552
Db 1434 GCCACATGAAGGTGACATGATGGTGAACA-----GAAGGAAGTGAAGTGGGAAGAC 1487
Qy 552 eTyrAspProGluGlnAsnAspGluHisIleGlyHisLeuAspAspArgSerLysProII 572
Db 1488 CCGGATCCACCTATTGGGCAGAGATTATGGCGTCTTTTCTTAATCCAGGAAGCTTAT 1547
Qy 572 eLeuPheSerMetAlaArgLeuAspArgValLysAsnIleThrGlyLeuValGluAlaPh 592
Db 1548 GATACTCGCACTTCTGAGGCTGATCCCAAGAGAACCTCACTACTTTAGTGAAGCAT 1607
Qy 592 eAlaLysCysAlaLysLeuArgGlnLeuValAsnLeuValValAlaGlyTyrAsnAs 612
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Qy 612 pValAsnLysSerLysAspArgGluGluIleAlaGluIleGluLysMetHisGluLeuII 632
Db 1668 TAATATCGCAAGATGCTAGCACCATTCTGCACCTCTTCTTCAATCTTGAAATGAT 1727
Qy 632 eLysThrHisAsnLeuPheGlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaAr 652
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Db 1845 TATTGAGCTTTTGGACTGACTTGTATTGAGCAGCAGCTTATGCTCTCCCAATGGTAGC 1904
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Db 2007 GGTTGCTGATAAGCAACTGTGGCTAAATGCAGGCAATGGATTAAAAATAATCCAC-- 2064
Qy 750 uLysTyrThrTrp-----LysIleTyrSerGluArgLeu 761
Db 2065 -CTTTCTCATGCCCGCAGCACTGTAAACTTATCTATCCGGATA 2109
RESULT 13
US-08-553-436A-5
? Sequence 5, Application US/08553436A
? Patent No. 5866790
? GENERAL INFORMATION:
? APPLICANT: HESSE, Holger
? APPLICANT: MULLER-ROBER, Bernd
? TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
? TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
? NUMBER OF INVENTION: CONCENTRATION
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Oetrolenk, Faber, Gerb & Soffen
? STREET: 1180 Avenue of the Americas
? CITY: New York
? STATE: NY
? COUNTRY: US
? ZIP: 10036-8403
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
```


CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,436A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01671
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4317596.1
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wellman, Edward
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Beta vulgaris
INDIVIDUAL ISOLATE: Saccharosephosphate Synthase
IMMEDIATE SOURCE:
LIBRARY: phage lamda zap
FEATURE:
NAME/KEY: CDS
LOCATION: 30..3167
US-08-553-436A-5

Alignment Scores:
Pred. No.: 3,81e-40 Length: 3635
Score: 441.50 Matches: 146
Percent Similarity: 45.50% Conservative: 102
Best Local Similarity: 26.79% Mismatches: 190
Query Match: 10.40% Indels: 107
DB: 2 Gaps: 24

US-10-080-114a-12 (1-809) x US-08-553-436A-5 (1-3635)

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QY 400 AlaGluLeuGinglyThr-----ProAspPheIleIleGlyAsnTyrSer 414
Db 909 GGTGAGCAAAATTGGTAGCGGGGAAACAGTTGGCCAGTTGCCATTCATGCACATATGCT 968
QY 415 AspGlyAsnLeuValAlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIle 434
Db 969 GATGCTGGTATTCTGCTGCTCTCTTCTTGGTGCCCTAAATGTTCCATGCTTTTAAACG 1028
QY 435 AlaHisAlaLeuGluLysThrLysTyrProAsp----- 445
Db 1029 GGGCATTTCTTGGCCGACAGCAAGTTAGACAGCTCTCTCAACACAGGGTCAATGTCTAAA 1088
QY 446 SerAspIlePheTyrLysAsnPheAspGluLysTyrHisPheSerCysGlnPheThrAla 465
Db 1089 GATGACATA-----AACATACATACAAAATAATGCTAGGATAGAGCC 1133
QY 466 AspIleIleAlaMetAsnAsnAlaAspPheIleIleThrSerThrTyrGlnGluIleAla 485
Db 1134 GAAGAGTTATCATTGATGCTCTGAGATAGTCATACTAGTACAAACAAGAAATAGAA 1193
QY 486 GlySerLysAsnThrValGlyGlnTyrGluSerHisThrAlaPheThrLeuProGlyLeu 505
Db 1194 -----GACCAATGGCCACTCTATGATGGGTTTGTAT---CCTGTGCTA 1232
QY 506 -----TyrArgValValHisGlyIleAspVal-----PheAspPro 517
Db 1233 GAACGTAAACTCCGTGCTAGGATGAGCGTGGTGAAGCTGTATGGAAGGTTTCATGCC 1292
QY 518 LysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGluLys 537
Db 1293 CGGATGGTTGTTATTCCTCTGGAATGGAATTCATCATATATTTCCACAT----- 1343
QY 538 AlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGluGln 557
Db 1344 -----GAGGCTGATATGATGCT-----GAAACAGAGAA 1373
QY 558 AsnAspGluHis-----IleGlyHisLeu 565
Db 1374 ACTGAAGAGCATCTTACATCATCCACTATCTGGGTGAGATTATGGCTCTCTTT 1433
QY 566 AspAspArgSerLysProIleLeuPheSerMetAlaArgLeuAspArgValLysAsnIle 585
Db 1434 TCTAAACCAAGAACCAATGATCTTGCCTTCTAGGCTGACCCGAGAGAAATATC 1493
QY 586 ThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeuArgGluLeuValAsnLeuVal 505
Db 1494 ACGACTTGGTCAAGCATTTGGAGATGCCGCTCCACTAAGGAGAGCTAGCTAATCTTACT 1553
QY 606 ValValAlaGlyTyrAsnAspValAsnLysSerLysAspArgGluGluIleAlaGluIle 625
Db 1554 CTTATAATGGGTAAACCGAGATGGTATTGACGAGATGTCACAGCAGTTCTTCAGTTCTC 1613
QY 626 GluLysMetHisGluLeuIleLysThrHisAsnLeuPheGlyGlnPheArgTyrPheSer 645
Db 1614 CTGTGAGTGTAAAGTAAATGATCAATACGACCTTTATGCTCAAGTAGCATAC---CCC 1670
QY 646 AlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArgTyrIleAlaAspThrHisGly 665
Db 1671 AAACATCAACAGCAAGCATGTTCTCGAGATTATCGTTTGGCAGCAACAGCAAGGGA 1730
QY 666 AlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeuThrValValGluAlaMetThr 685
Db 1731 GTCTTTTAAATCAAGCTTTTATGAGCCATTGGGCTGACTCTTAATAGAGGACAGACT 1790
QY 686 CysGlyLeuProThrPheAlaThrLeuHisGlyGlyProAlaGluIleIleGluHisGly 705
Db 1791 CATGTTTACCGATGGTGTCTACGAAAAATGGAGCCCTGTTGTATATCCAGAGGCTCCT 1850
QY 706 ValSerGlyPheHisIleAspProTyrHisProGluGlnAlaVal----- 720
Db 1851 GATAATGCTCTCTTGTGGATCTCT---CATGAGCAGCAGCTATTGTCTACTGCTTTGCTG 1907
QY 721 AsnLeuMetAlaAsp-----PhePheAspArgCysLysGlnAspProAspHisTyrVal 738
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Db 1908 AAGCTTGTCTCATAGCAACTATGACAAAATGCCAGCAAAAT 1952
Qy 739 AsnIleSerGlyAlaGlyLeuGlnAArgIleTyrGluYstYrThrTyrLysIleTyrSer 758
Db 1953 -----GACTGAAATAATATTCAT---CTCTACTCTTGGCCAGAGCAATTCG 1994
Qy 759 GluArgLeuMetThr 763
Db 1995 AAGACATACCTACTCT 2009
RESULT 14
US-08-429-054A-12
Sequence 12, Application US/38429054A
Patent No. 5917126
GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: French 96402094.9
FILING DATE: 20-July-1990
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Charles A. Musierlian
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509
TYPE: Nucleic acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
US-08-429-054A-12
Alignment Scores:
Pred. No.: 1,55e-39 Length: 3509
Score: 436.00 Matches: 161
Percent Similarity: 40.79% Conservative: 96
Best Local Similarity: 25.56% Mismatches: 209
Query Match: 10.27% Indels: 164
DB: 2 Gaps: 26
US-10-080-114A-12 (1-809) x US-08-429-054A-12 (1-3509)

Qy 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
Db 532 GGAGACACCATCGAGAGCTT-----GCG 555
Qy 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276
Db 556 CCGGTTGAGACGACCAAGAAGAGTTCACAGAGAACTTCTCTGACCTTACCGTCTGGTCT 615
Qy 277 -----PheAsnValValValSerProHisGlyTyrPhe----- 288
Db 616 GACGACAAATAGGAGAGAAAGCTTTACATTGTGTCTCATCGCGTCATGGTCTTGTCT 675
Qy 289 GlyClnAlaAsnValLeuGluLeu-----ProAspThrGlyGlyGlnIleValTyrIleLeu 307
Db 676 GGAGAAACATGGAACTAGGTCTGTGATCTGTATACAGGTGGCCAGGTGAATATGTGGTC 735
Qy 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysGlnGlyLeuAsp 327
Db 736 GAACCTTGAAGAGCG-----ATGTC 756
Qy 328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp----- 341
Db 757 ATGATGCTCGAGGTGTACAGGGTGGACCTCTTCACTCGTCAAGTGTCACTCTCCGACGTG 816
Qy 342 -----AlaLysGlyThrSerCysAsnGlnArg 350
Db 817 GACTGGAGCTACGGTGAGCCAAACCGAGATGTATGCGCGGTTCCATGATGGAGAGGG 876
Qy 351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
Db 877 ATGGGTGAGAGTGGCGGA-----GCCTACATTGTGGCATACCGTGT----- 918
Qy 371 AsnGlyIleLeuLysTyrIleSerArgPheAspValTyrProTyrLeuGluThrPhe 390
Db 919 ---GGGCGCGGGATTAATACCTCAAGAGAGCGTTGTGGCTTACCTCCAAAGAGTT 975
Qy 391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
Db 976 GTCGATGGAGCCCTTGGCATATCTGAAACATGTCCCAAGGCTCTGGGAGAGAGAGTTGGA 1035
Qy 405 -----ThrProAspPheIleGlyAsnTyrSerAspGlyAsnLeuVal 419
Db 1036 ATTGGGAGGCGCAGTACTACTCTTACGTGATACATGCGGCATATGCGCATGTGGAGATGT 1095
Qy 420 AlaSerLeuLeuSerTyrLysMetGlyIleThrClnCysAsnIleAlaHisAlaLeuGlu 439
Db 1096 GCTGCTCTCTTCTTGTGGTGGCTGAATGTGCCAATGTGTCTCACTGGCCACTCACTTGGG 1155
Qy 440 LysThrIys-----TyrProAspSerAspIlePheTyrLysAsnPheAspGlu 455
Db 1156 AGGACAAAGCTGGAGCAACAACTGCTGAAGCAAGGCGCATGTCCAAGGAGAGAGATCGTTCG 1215
Qy 456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe 475
Db 1216 ACATACAGATCATGAGGCGTATCGAGGGTGAAGAGCTGGCCCTGGATGGTGGAGAGCTT 1275
Qy 476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
Db 1276 GTAATCAGGAGCAAGGCGAGAGATTGAT-----GAGCAGTGG----- 1314
Qy 496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal----- 514
Db 1315 -----GGATTGTAC-----GATGATTGATGTCAG 1341
Qy 515 -----PheAsp 516
Db 1342 CTTGAGAAAGTGTGAGGCGCAGCGGAGCGGGGTAGTCTGCCATGGTCTGCTTACATG 1401
Qy 517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
Db 1402 CTTAGGATGGTGTGATCTCTCCGGAATGGATTTCAGCAATGTGTAGTTCAT----- 1455

Qy	520	AsnLeuValSerProGlyAlaAspMetSerIleTyrPheProHisThrGluLysAlaLys	539
Db	1355	GCACAAATCCACCTGGTATGGAGTTCCATCATATTGTCACAC	1399
Qy	540	ArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGluGinAsnAsp	559
Db	1400	-----GATGGTGATATGAGAGT-----GACCCGAGGAATTTG	1435
Qy	560	GluHisIleGlyHisLeuAsp-----Asp	567
Db	1436	GATCATCTGCCGCCCAAGATCCACCTATTGGTCGAGATAATGCGCTTCITTAACCAAC	1495
Qy	568	ArgSerIysProIleLeuPheSerMetAlaArgLeuAspArgValIysAsnIleThrGly	587
Db	1496	CTTCGCAAGCCTATGATACTTGTCTCGCTAGACAGACCCCTAAAGACATCATCAAACT	1555
Qy	588	LeuValGluAlaPheAlaLysCysAlaLysLeuArgGluLeuValAsnLeuValVal	607
Db	1556	TTGGTAAAGCAATTTGGAGAATGCCGTCCTTCAAGAGCTTGCCAACTTACATPANTT	1615
Qy	608	AlaGlyTyrAsnAspValAsnLysSerLysAspArgGluGluIleAlaGluIleGluLys	627
Db	1616	ATGCGTAACCGAGATGGAATTTGATGAGATGTCAAGCAAAATGCTTCTGTCTTCTCTCG	1675
Qy	628	MetHisGluLeuIleLysThrHisAsnLeuPheGlyGlnPheArgTrpIleSerAlaGln	647
Db	1676	GTACTTAAGTTGATTGACAGATGATCTGTATGGCAATGGCATAT-----CCTAAACAT	1732
Qy	648	ThrAsnArgAlaArgAsnGlyGluLeuTyrArgTyrIleAlaAspThrHisGlyAlaPhe	667
Db	1733	CACAAACAATATGATGTTCTCGCATATATCGCCTAGCAGCAAGACAAAGGGTGTTC	1792
Qy	668	ValGlnProAlaLeuTyrGluAlaPheGlyLeuThrValValGluAlaMetThrCysGly	687
Db	1793	ATTAATCCAGCTTTCATGTAGCAATTTGGTCTTACCTTAATTGAGGCAGCTGCTCATGGT	1852
Qy	688	LeuProThrPheAlaThrLeuHisGlyGlyProAlaGluIleIleGluHisGlyVal	706
Db	1853	TTGCCAATTTGTGACTAAATTTGGAGGTCCTGTTGATNT-----CATAGGGTACTT	1906
Qy	707	---SerGlyPheHisIleAspProTyrHisProGluGlnAlaValAsnLeuMetalAsp	725
Db	1907	GACAAATGGTCTGCTCGTAGATCCC---CATGATCCAGCTCTATT-----GCTGAT	1954
Qy	726	PhePheAspArgCysLysGlnAspProAspHisTrpValAsnIleSerGlyAlaGlyLeu	745
Db	1955	GCTCTTTTGAAGCTTGTATGACAAACAACAACTTTGGGCAAAATGTAGACAGAAATGGGTTA	2014
Qy	746	GlnArgIleTyrGluLysTyrThrTrp-----LysIleTyrSerGluArgLeu	761
Db	2015	AAGNAATATTCAT---TTATTTTATGCCCGAGCAGCTGTAAAGTACTTCTTCTTAAATA	2071
Qy	762	MetThrLeuAlaGlyValTyrGlyPheTrpLys	772
Db	2072	GCACATGCAAGCCCAAGGCATTCACATGCGAC	2104